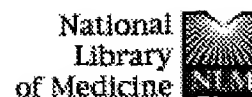


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
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



















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
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
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










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
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
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
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
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
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
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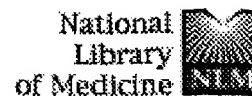


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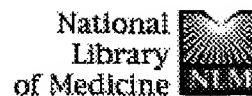
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
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
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
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
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
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
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




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















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





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
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
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
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
















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
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
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
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
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
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
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
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
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
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
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
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
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
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
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CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

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=> s hGrb14
56 FILES SEARCHED...
L1 10 HGRB14

=> DUP REM L1
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,
DRUGMONOG2, IMSRESEARCH, FEDRIP, FOREGE, GENBANK, IMSPRODUCT, KOSMET,
MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L1
L2 4 DUP REM L1 (6 DUPLICATES REMOVED)

=> D L2 1-4

L2 ANSWER 1 OF 4 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
Learning Company; All Rights Reserved on STN
AN 2003:59360 DISSABS Order Number: AAIMQ76780
TI The role of the ***hGRB14*** adaptor protein BPS domain in insulin
signaling
AU Kelly, Sherrie Lynne [M.Sc.]; Triggs-Raine, Barbara [advisor]
CS The University of Manitoba (Canada) (0303)
SO Masters Abstracts International, (2003) Vol. 41, No. 5; p. 1378. order
No.: AAIMQ76780. 126 pages.
ISBN: 0-612-76780-9.

DT Dissertation
FS MAI
LA English
ED Entered STN: 20031201
Last Updated on STN: 20031201

L2 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 2001:128080 BIOSIS
DN PREV200100128080
TI Human growth factor receptor bound 14 binds the activated insulin receptor
and alters the insulin-stimulated tyrosine phosphorylation levels of
multiple proteins.
AU Hemming, Richard; Agatep, Ronald; Badiani, Ketan; Wyant, Kerrie; Arthur,
Gilbert; Gietz, R. Daniel; Triggs-Raine, Barbara [Reprint author]
CS Department of Biochemistry and Medical Genetics, University of Manitoba,
770 Bannatyne Avenue, Winnipeg, MB, R3E 0W3, Canada
traine@ms.umanitoba.ca
SO Biochemistry and Cell Biology, (2001) Vol. 79, No. 1, pp. 21-32. print.
CODEN: BCBIEQ. ISSN: 0829-8211.
DT Article
LA English
ED Entered STN: 14 Mar 2001
Last Updated on STN: 15 Feb 2002

L2 ANSWER 3 OF 4 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
Learning Company; All Rights Reserved on STN
AN 2001:38658 DISSABS Order Number: AAIMQ51679
TI The insulin signaling pathway: Evidence that Tax1bp1/Txbp151 is a dimeric
human Grb14 interacting protein
AU Agatep, Ronald [M.Sc.]; Gietz, R. D. [adviser]
CS The University of Manitoba (Canada) (0303)
SO Masters Abstracts International, (2000) Vol. 39, No. 1, p. 151. Order No.:
AAIMQ51679. 143 pages.
ISBN: 0-612-51679-2.
DT Dissertation
FS MAI
LA English

L2 ANSWER 4 OF 4 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2000:576640 SCISEARCH
GA The Genuine Article (R) Number: 313NK
TI Effect of overexpression of ***hGrb14*** on Akt kinase and insulin
signalling
AU Badiani K (Reprint); Hemming R; Gietz R D; TriggsRaine B
SO DIABETES, (MAY 2000) Vol. 49, Supp. [1], pp. 1359-1359.
Publisher: AMER DIABETES ASSOC, 1660 DUKE ST, ALEXANDRIA, VA 22314.
ISSN: 0012-1797.
DT Conference; Journal
FS LIFE; CLIN
LA English
REC Reference Count: 0

=> S Grb14 OR Grb10 OR Grb7
52 FILES SEARCHED...
L3 1778 GRB14 OR GRB10 OR GRB7

=> DUP REM L3
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,
DRUGMONOG2, IMSRESEARCH, FEDRIP, FOREGE, GENBANK, IMSPRODUCT, KOSMET,
MEDICONF, NUTRACEUT, PCTGEN, PHAR, PHARMAML, RDISCLOSURE, SYNTHLINE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
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PROCESSING COMPLETED FOR L3
L4 907 DUP REM L3 (871 DUPLICATES REMOVED)

=> S Grb14
L5 318 GRB14

=> DUP REM L5
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,
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ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L5

=> D L6 1-135

- L6 ANSWER 1 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
 AN 2003:1051167 SCISEARCH
 GA The Genuine Article (R) Number: 746XW
 TI Grb10 exceeding the boundaries of a common signaling adapter
 AU Riedel H (Reprint)
 CS Wayne State Univ, Dept Biol Sci, 2171 BSB, Detroit, MI 48202 USA
 (Reprint); Wayne State Univ, Dept Biol Sci, Detroit, MI 48202 USA
 CYA USA
 SO FRONTIERS IN BIOSCIENCE, (JAN 2004) Vol. 9, pp. 603-618.
 Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
 BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
 ISSN: 1093-9946.
 DT General Review; Journal
 LA English
 REC Reference Count: 105
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
- L6 ANSWER 2 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
 AN 2003:1051148 SCISEARCH
 GA The Genuine Article (R) Number: 746XW
 TI Grb10: More than a simple adaptor protein
 AU Lim M A; Riedel H; Liu F (Reprint)
 CS Univ Texas, Hlth Sci Ctr, Dept Pharmacol, 7703 Floyd Curl Dr, San Antonio,
 TX 78229 USA (Reprint); Univ Texas, Hlth Sci Ctr, Dept Pharmacol, San
 Antonio, TX 78229 USA; Wayne State Univ, Dept Biol Sci, Detroit, MI 48202
 USA
 CYA USA
 SO FRONTIERS IN BIOSCIENCE, (JAN 2004) Vol. 9, pp. 387-403.
 Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
 BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
 ISSN: 1093-9946.
 DT General Review; Journal
 LA English
 REC Reference Count: 103
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
- L6 ANSWER 3 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
 AN 2003:1051131 SCISEARCH
 GA The Genuine Article (R) Number: 746XW
 TI Grb7 in intracellular signaling and its role in cell regulation
 AU Shen T L; Guan J L (Reprint)
 CS Cornell Univ, Dept Mol Med, Ithaca, NY 14853 USA (Reprint)
 CYA USA
 SO FRONTIERS IN BIOSCIENCE, (JAN 2004) Vol. 9, pp. 192-200.
 Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
 BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
 ISSN: 1093-9946.
 DT Article; Journal
 LA English
 REC Reference Count: 86
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
- L6 ANSWER 4 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
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 AN 2003:43622 DISSABS Order Number: AAI3075524
 TI Structural and functional analysis of the BPS and SH2 domains of Grb10
 AU Stein, Evan Gary [Ph.D.]; Hubbard, Stevan R. [advisor]
 CS New York University (0146)
 SO Dissertation Abstracts International, (2003) Vol. 63, No. 12B, p. 5687.
 Order No.: AAI3075524. 91 pages.
 ISBN: 0-493-95827-4.
 DT Dissertation
 FS DAI
 LA English
- L6 ANSWER 5 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
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 AN 2003:59360 DISSABS Order Number: AAIMQ76780
 TI The role of the hGRB14 adaptor protein BPS domain in insulin signaling
 AU Kelly, Sherrie Lynne [M.Sc.]; Triggs-Raine, Barbara [advisor]
 CS The University of Manitoba (Canada) (0303)
 SO Masters Abstracts International, (2003) Vol. 41, No. 5, p. 1378. Order

No.: AAIMQ76780. 126 pages.

ISBN: 0-612-76780-9.

DT Dissertation
FS MAI
LA English
ED Entered STN: 20031201
Last Updated on STN: 20031201

L6 ANSWER 6 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2003:761870 CAPLUS
DN 139:287335

TI Gene expression profiling in the brain of rat models and use of nucleotide
sequences as gene chips for screening antidepressants
IN Yoshikawa, Takeo; Nakaya, Noriaki; Aburaya, Hiroyuki
PA Institute of Physical and Chemical Research, Japan
SO Jpn. Kokai Tokkyo Koho, 18 pp.
CODEN: JKXXAF

DT Patent
LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2003274949	A2	20030930	JP 2002-81502	20020322
PRAI	JP 2002-81502		20020322		

L6 ANSWER 7 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 2
AN 10399185 IFIPAT;IFIUDB;IFICDB
TI DIAGNOSIS OF DISEASES ASSOCIATED WITH THE IMMUNE SYSTEM BY DETERMINING
CYTOSINE METHYLATION

IN Berlin Kurt (DE); Olek Alexander (DE); Piepenbrock Christian (DE)
PA Unassigned Or Assigned To Individual (68000)

PI US 2003143606 A1 20030731
AI US 2002-311455 20021216
WO 2001-EP7537 20010702
20021216 PCT 371 date
20021216 PCT 102(e) date

PRAI DE 2000-10032529 20000630
DE 2000-10043826 20000901

FI US 2003143606 20030731

DT Utility; Patent Application - First Publication

FS CHEMICAL
APPLICATION

CLMN 31

L6 ANSWER 8 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 3
AN 10385219 IFIPAT;IFIUDB;IFICDB
TI GDU, A NOVEL SIGNALLING PROTEIN

IN Daly Roger John (AU); Sutherland Robert Lyndsay (AU)

PA Unassigned Or Assigned To Individual (68000)

PI US 2003129639 A1 20030710

AI US 2002-323001 20021218

RLI WO 1996-AU258 19960502 Section 371 PCT Filing UNKNOWN

US 1998-945771 19980422 DIVISION 6465623

US 2002-242332 20020911 DIVISION

PRAI AU 1995-2742 19950502

FI US 2003129639 20030710

US 6465623

DT Utility; Patent Application - First Publication

FS CHEMICAL
APPLICATION

CLMN 9

GI 3 Figure(s).

FIG. 1 shows a schematic representation of *****Grb14***** structure with a restriction map for the *****Grb14***** cDNA and the cDNA clones used to derive the *****Grb14***** sequence aligned underneath. The initial clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening using clone 1 as a probe. The *****Grb14***** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of *****Grb14*****. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp.

FIG. 3 shows the sequence homology between *****Grb14*****, Grb7, Grb10

and F10E9.6. As alignment of the amino acid sequences of ***Grb14*** , mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 9 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 4

AN 10360583 IFIPAT;IFIUDB;IFICDB

TI METHODS AND COMPOSITIONS FOR INHIBITING GRB7

IN Krag David N; Oligino Lyn; Pero Stephanie C

PA Unassigned Or Assigned To Individual (68000)

PI US 2003105000 A1 20030605

AI US 2001-13815 20011105

PRAI US 2000-245755P 20001103 (Provisional)

FI US 2003105000 20030605

DT Utility; Patent Application - First Publication

FS CHEMICAL

APPLICATION

CLMN 93

GI 16 Figure(s).

FIG. 1 is a histogram showing the binding of Grb7 binding peptides (G7BP) to the SH2 domain of human Grb7 by ELISA.

FIG. 2 is a histogram showing the binding of a control phage clone to the SH2 domain of Grb2 but not to the SH2 domain of Grb7.

FIG. 3 is a histogram showing the effect of mutation on a G7BP-4 phage clone on its ability to bind to the SH2 domain of Grb7.

FIG. 4 is a histogram showing the binding specificity of seven Grb7 binding peptides to the SH2 domains of Grb7, Grb7 beta D5beta D6, ***Grb14***, full length Grb2, and BSA using a phage ELISA.

FIG. 5A is a graph showing the inhibition of G7-18 peptide-phage binding to Grb7-SH2 with the free synthetic peptides G7-18, G718NATE and G7-8.

FIG. 5B is a graph showing the inhibition of G7-8NA peptide-phage binding to Grb7-SH2 with the free synthetic peptides G7-8, G7-8NA and G7-8NATE.

FIG. 6A is a graph showing G7-18NATE inhibits the association of Grb7 with the ErbB family of receptors, as detected by antiphosphotyrosine.

FIG. 6B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software, showing G7-18NATE inhibits the association of Grb7, not Grb2, with the ErbB family in a dose-dependent manner.

FIG. 7A is a graph showing that G7-18NATE inhibits the association of Grb7 with ErbB3 specifically in a dose-dependent manner, as detected by anti-ErbB3.

FIG. 7B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing that G7-18NATE inhibits the association of Grb7 with ErbB3 in a dose-dependent manner.

FIG. 8A is a graph showing that G7-18NATE inhibits the association of Grb7 with ErbB2 specifically in a dose-dependent manner, as detected by anti-ErbB2.

FIG. 8B is a densitometric analysis of autoradiographs using the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing that G7-18NATE inhibits the association of Grb7 with ErbB2 in a dose-dependent manner.

FIG. 9A is one possible chemical structure for G7BP-4NATE (SEQ ID NO:50). Other thioether linkages are illustrated in FIGS. 9B, 9C, 9D and 9E, and it is to be understood that any of these linkages can be used in the formation of G7BP-4NATE.

FIG. 9B is the structure of a thioether containing peptide (G1TE). This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9C is another possible structure for the thioether containing peptide GI TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9D is another possible structure for the thioether containing peptide G1TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

FIG. 9E is another possible structure for the thioether containing peptide GI TE. This structure illustrates one possible thioether linkage between the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.

L6 ANSWER 10 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 5
AN 10300425 IFIPAT;IFIUDB;IFICDB
TI GDU, A NOVEL SIGNALLING PROTEIN
IN Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
PA Unassigned Or Assigned To Individual (68000)
PI US 2003044834 A1 20030306
AI US 2002-242332 20020911
RLI WO 1996-AU258 19960502 Section 371 PCT Filing UNKNOWN
US 1998-945771 19980422 DIVISION 6465623
PRAI AU 1995-2742 19950502
FI US 2003044834 20030306
US 6465623

DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION

CLMN 9

GI 3 Figure(s).

FIG. 1 shows a schematic representation of *****Grb14***** structure with a restriction map for the *****Grb14***** cDNA and the cDNA clones used to derive the *****Grb14***** sequence aligned underneath. The initial clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening using clone 1 as a probe. The *****Grb14***** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; AV; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.

FIG. 2 shows the nucleotide and amino acid sequence of *****Grb14*****. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp.

FIG. 3 shows the sequence homology between *****Grb14*****, Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of *****Grb14*****, mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 11 OF 135 USPATFULL on STN
AN 2003:330145 USPATFULL
TI Skin cell biomarkers and methods for identifying biomarkers using nucleic acid microarrays
IN Dooley, Thomas P., Vestavia Hills, AL, UNITED STATES
Curto, Ernest V., Huntsville, AL, UNITED STATES
Davis, Richard L., JR., Homewood, AL, UNITED STATES
PI US 2003232356 A1 20031218
AI US 2003-361006 A1 20030210 (10)
PRAI US 2002-354519P 20020208 (60)
DT Utility
FS APPLICATION
LN.CNT 1897
INCL INCLM: 435/006.000
INCLS: 702/020.000
NCL NCLM: 435/006.000
NCLS: 702/020.000
IC [7]
ICM: C12Q001-68
ICS: G06F019-00; G01N033-48; G01N033-50

L6 ANSWER 12 OF 135 USPATFULL on STN
AN 2003:225702 USPATFULL
TI Polynucleotide encoding a novel pleckstrin homology domain and proline rich domain containing adapter protein, PMN29
IN Finger, Joshua N., San Marcos, CA, UNITED STATES
Perez-Villar, Juan J., Mercerville, NJ, UNITED STATES
Rajashekar, Reddy, Langhorne, PA, UNITED STATES
Yang, Guchen, Morrisville, PA, UNITED STATES
Kiener, Peter A., Doylestown, PA, UNITED STATES
PI US 2003157514 A1 20030821
AI US 2002-234816 A1 20020904 (10)
PRAI US 2001-317063P 20010904 (60)
DT Utility
FS APPLICATION
LN.CNT 13865

INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
435/007.200
NCL NCLM: 435/006.000
NCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
435/007.200
IC [7]
ICM: C12Q001-68
ICS: G01N033-53; G01N033-567; C07H021-04; C12P021-02; C12N005-06;
C07K014-47

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 13 OF 135 USPATFULL on STN
AN 2003:37578 USPATFULL
TI Specimen-linked G protein coupled receptor database
IN Muraca, Patrick J., Pittsfield, MA, UNITED STATES
PI US 2003027223 A1 20030206
AI US 2002-184694 A1 20020628 (10)
PRAI US 2001-302316P 20010629 (60)
DT Utility
FS APPLICATION
LN.CNT 3618
INCL INCLM: 435/007.210
INCLS: 702/019.000
NCL NCLM: 435/007.210
NCLS: 702/019.000
IC [7]
ICM: G01N033-567
ICS: G06F019-00; G01N033-48; G01N033-50

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 14 OF 135 USPATFULL on STN
AN 2003:222015 USPATFULL
TI Compositions for the detection of blood cell and immunological response
gene expression
IN Cocks, Benjamin G., Sunnyvale, CA, United States
Stuart, Susan G., Montara, CA, United States
Seilhamer, Jeffrey J., Los Altos Hills, CA, United States
PA Incyte Corporation, Palo Alto, CA, United States (U.S. corporation)
PI US 6607879 B1 20030819
AI US 1998-23655 19980209 (9)
DT Utility
FS GRANTED
LN.CNT 3719
INCL INCLM: 435/006.000
INCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
536/024.320; 536/024.330
NCL NCLM: 435/006.000
NCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
536/024.320; 536/024.330
IC [7]
ICM: C12Q001-68
ICS: C07H021-00
EXF 435/6; 435/69.1; 536/22.1; 536/23.1; 536/24.1; 536/24.3-24.33
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 15 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2003:254017 BIOSIS
DN PREV200300254017
TI Structural basis for dimerization of the Grb10 Src homology 2 domain.
Implications for ligand specificity.
AU Stein, Evan G.; Ghirlando, Rodolfo; Hubbard, Stevan R. [Reprint Author]
CS Skirball Institute of Biomolecular Medicine, New York University School of
Medicine, 540 First Ave., New York, NY, 10016, USA
hubbard@saturn.med.nyu.edu
SO Journal of Biological Chemistry, (April 11, 2003) Vol. 278, No. 15, pp.
13257-13264. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 28 May 2003
Last Updated on STN: 28 May 2003

L6 ANSWER 16 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7

AN 2003:355616 BIOSIS
DN PREV200300355616
TI NIK is a component of the EGF/hereregulin receptor signaling complexes.
AU Chen, Danying; Xu, Liang-Guo; Chen, Lei; Li, Lixia; Zhai, Zhonghe; Shu, Hong-Bing [Reprint Author]
CS Department of Immunology, National Jewish Medical and Research Center, University of Colorado Health Sciences Center, 1400 Jackson Street, K516c, Denver, CO, 80206, USA
shuh@njc.org
SO Oncogene, (10 July, 2003) Vol. 22, No. 28, pp. 4348-4355. print.
ISSN: 0950-9232 (ISSN print).
DT Article
LA English
ED Entered STN: 6 Aug 2003
Last Updated on STN: 6 Aug 2003

L6 ANSWER 17 OF 135 LIFESCI COPYRIGHT 2004 CSA on STN
AN 2003:53872 LIFESCI
TI The Grb10/Nedd4 Complex Regulates Ligand-Induced Ubiquitination and Stability of the Insulin-Like Growth Factor I Receptor
AU Vecchione, A.; Marchese, A.; Henry, P.; Rotin, D.; Morrione, A.*
CS Department of Urology and Kimmel Cancer Center, Thomas Jefferson University, BLSB Room 631, 233 South 10th St., Philadelphia, PA 19107; E-mail: Andrea.Morrione@mail.tju.edu
SO Molecular and Cellular Biology [Mol. Cell. Biol.], (20030500) vol. 23, no. 9, pp. 3363-3372.
ISSN: 0270-7306.
DT Journal
FS G
LA English
SL English

L6 ANSWER 18 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:476188 BIOSIS
DN PREV200300476188
TI Characterization of a novel gene (HGPI) potentially involved in osteosarcoma progression.
AU Eppert, Kolja [Reprint Author]; Aneliunas, Vicky [Reprint Author]; Wunder, Jay S. [Reprint Author]; Andrulis, Irene L. [Reprint Author]
CS Fred A. Litwin Centre for Cancer Genetics, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, ON, Canada
SO Proceedings of the American Association for Cancer Research Annual Meeting, (July 2003) Vol. 44, pp. 1041-1042. print.
Meeting Info.: 94th Annual Meeting of the American Association for Cancer Research. Washington, DC, USA. July 11-14, 2003.
ISSN: 0197-016X.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 15 Oct 2003
Last Updated on STN: 15 Oct 2003

L6 ANSWER 19 OF 135 BIOTECHNO COPYRIGHT 2004 Elsevier Science B.V. on STN
DUPLICATE
AN 2003:37386423 BIOTECHNO
TI Using gene expression profiling to identify the molecular basis of the synergistic actions of hepatocyte growth factor and vascular endothelial growth factor in human endothelial cells
AU Gerritsen M.E.; Tomlinson J.E.; Zlot C.; Ziman M.; Hwang S.
CS M.E. Gerritsen, 541 Parrott Drive, San Mateo, CA 94402, United States.
E-mail: meg570@comcast.net
SO British Journal of Pharmacology, (2003), 140/4 (595-610), 52 reference(s)
CODEN: BJPCBM ISSN: 0007-1188
DT Journal; Conference Article
CY United Kingdom
LA English
SL English

L6 ANSWER 20 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 2003:451765 BIOSIS
DN PREV200300451765
TI Carcinogen mediated initiation of glial progenitors in the rat brain results in marked dependency of proliferation and differentiation by insulin and FGF-2.
AU Kokkinakis, Demetrius Michael [Reprint Author]; Yang, Shuting [Reprint

Author]
CS University of Pittsburgh, Pittsburgh, PA, USA
SO Proceedings of the American Association for Cancer Research Annual Meeting, (July 2003) Vol. 44, pp. 482. print.
Meeting Info.: 94th Annual Meeting of the American Association for Cancer Research. Washington, DC, USA. July 11-14, 2003.
ISSN: 0197-016X.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 1 Oct 2003
Last Updated on STN: 1 Oct 2003

L6 ANSWER 21 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 2003:587917 BIOSIS
DN PREV200300570714
TI The PIR domain of ***Grb14*** is an intrinsically unstructured protein: Implication in insulin signaling.
AU Moncoq, Karine; Broutin, Isabelle [Reprint Author]; Larue, Valery; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly, Edith; Burnol, Anne-Francoise; Ducruix, Arnaud
CS Laboratoire de Cristallographie et RMN Biologiques, Faculte de Pharmacie Paris 5, 4 avenue de l'Observatoire, 75270, Paris Cedex, 06, France
broutin@pharmacie.univ-paris5.fr
SO FEBS Letters, (20 November 2003) Vol. 554, No. 3, pp. 240-246. print.
CODEN: FEBLAL. ISSN: 0014-5793.
DT Article
LA English
ED Entered STN: 10 Dec 2003
Last Updated on STN: 10 Dec 2003

L6 ANSWER 22 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11
AN 2003:390017 BIOSIS
DN PREV200300390017
TI Inhibition of FGF receptor signalling in Xenopus oocytes: Differential effect of Grb7, Grb10 and ***Grb14***.
AU Cailliau, Katia; Le Marcis, Veronique; Bereziat, Veronique; Perdereau, Dominique; Cariou, Bertrand; Vilain, Jean Pierre; Burnol, Anne-Francoise; Browaeys-Poly, Edith [Reprint Author]
CS Laboratoire de Biologie du Developpement, Universite des sciences; Technologies de Lille, UPRES UA 1033, IFR 118, Batiment SN3, Villeneuve d'Ascq Cedex, France
edith.browaeys@univ-lille1.fr
SO FEBS Letters, (31 July, 2003) Vol. 548, No. 1-3, pp. 43-48. print.
CODEN: FEBLAL. ISSN: 0014-5793.
DT Article
LA English
ED Entered STN: 27 Aug 2003
Last Updated on STN: 27 Aug 2003

L6 ANSWER 23 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 12
AN 10142689 IFIPAT;IFIUDB;IFICDB
TI GDU, A NOVEL SIGNALLING PROTEIN; IT MAY PROVIDE A TARGET IN DISEASES OR CONDITIONS IN WHICH PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) PLAYS A REGULATORY ROLE E.G. WOUND HEALING, FIBROTIC CONDITIONS, ATHEROSCLEROSIS
IN DALY ROGER JOHN (AU); SUTHERLAND ROBERT LINDSAY (AU)
PA Unassigned Or Assigned To Individual (68000)
PPA Garvan Institute of Medical Research AU (Probable)
PI US 2002086328 A1 20020704
AI US 1998-945771 19980422
WO 1996-US258 19960502
FI US 2002086328 20020704
US 6465623 20021015
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 9
GI 3 Figure(s).
FIG. 1 shows a schematic representation of ***Grb14*** structure with a restriction map for the ***Grb14*** cDNA and the cDNA clones used to derive the ***Grb14*** sequence aligned underneath. The initial clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening

using clone 1 as a probe. The ***Grb14*** cDNA sequence was completed using two clones L5 and L6, isolated from a human liver cDNA library. Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp. FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***. The PH domain is underlined and the SH2 domain indicated by bold type. The translation termination codon is shown by an asterisk in the amino acid sequence. Numbers refer to distances in bp. FIG. 3 shows the sequence homology between ***Grb14***, Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***, mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

L6 ANSWER 24 OF 135 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 13
 AN 10094016 IFIPAT;IFIUDB;IFICDB
 TI POTENTIAL EFFECTOR FOR THE GRB7 FAMILY OF SIGNALLING PROTEINS; NUCLEOTIDE SEQUENCES CODING SIGNAL TRANSDUCTION POLYPEPTIDE; FOR USE IN THE DIAGNOSIS AND TREATMENT OF CANCERS
 IN DALY ROGER JOHN (AU); SUTHERLAND ROBERT L (AU)
 PA Unassigned Or Assigned To Individual (68000)
 PI US 2002037582 A1 20020328
 AI US 2000-509196 20000323
 WO 1998-AU795 19980923
 PRAI AU 1997-9388 19970923
 FI US 2002037582 20020328
 DT Utility; Patent Application - First Publication
 FS CHEMICAL APPLICATION
 CLMN 15
 GI 2 Figure(s).

FIG. 1 provides the nucleotide and amino acid (single letter code) sequence of 2.2412. Numbers refer to distances in base pairs. Ankyrin-type repeat sequences are underlined. An additional repeat sequence is indicated by italics. The stop codon is represented by all asterisk. The original cDNA clone 2.2412 isolated by the two hybrid screen spans nucleotides 6942664 of this sequence. FIG. 2 provides a map of the 2.2412-binding region on ***Grb14***. A. Structure of the deletion constructs used in the analysis. Gal4 DNA-BD fusion constructs encoding full length ***Grb14*** (FL), the Nterminal (N), central region (C) and N-terminal+central region (N+C) were generated in the vector pAS2.1. B. Results of betagalactosidase activity assays following transformation of the above plasmids into yeast strain Y190 together with the original 2.2412 cDNA clone in pACT-2.

L6 ANSWER 25 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2002:10730 CAPLUS
 DN 136:49326
 TI Diagnosis of diseases associated with the immune system using oligomer probes to detect cytosine methylation state
 IN Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt
 PA Epigenomics A.-G., Germany
 SO PCT Int. Appl., 32 pp.
 CODEN: PIXXD2
 DT Patent
 LA German
 FAN.CNT 68

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002000928	A2	20020103	WO 2001-EP7537	20010702
	WO 2002000928	A3	20020801		
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
DE	10032529	A1	20020207	DE 2000-10032529	20000630
EP	1274865	A2	20030115	EP 2001-953936	20010406

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 JP 2003531589 T2 20031028 JP 2001-575634 20010406
 EP 1360319 A2 20031112 EP 2001-955278 20010406
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 EP 1294951 A2 20030326 EP 2001-967115 20010702
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
 DE 20121966 U1 20031224 DE 2001-20121966 20010702
 US 2003143606 A1 20030731 US 2002-311455 20021216
 US 2003162194 A1 20030828 US 2003-240452 20030414
 PRAI DE 2000-10032529 A 20000630
 DE 2000-10043826 A 20000901
 DE 2000-10019058 A 20000406
 DE 2000-10019173 A 20000407
 WO 2001-EP3969 W 20010406
 WO 2001-EP4016 W 20010406
 EP 2001-967115 A 20010702
 WO 2001-EP7537 W 20010702

L6 ANSWER 26 OF 135 USPATFULL on STN
 AN 2002:315083 USPATFULL
 TI Nucleic acid sequences associated with baldness
 IN Pritchard, David, Seattle, WA, UNITED STATES
 Burmer, Glenna, Seattle, WA, UNITED STATES
 Brown, Joseph, Seattle, WA, UNITED STATES
 Demas, Vasiliki, Seattle, WA, UNITED STATES
 PI US 2002177566 A1 20021128
 AI US 2001-825096 A1 20010402 (9)
 PRAI US 2000-199745P 20000425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 3768
 INCL INCLM: 514/044.000
 INCLS: 435/006.000; 435/007.210; 424/070.100
 NCL NCLM: 514/044.000
 NCLS: 435/006.000; 435/007.210; 424/070.100
 IC [7]
 ICM: A61K048-00
 ICS: C12Q001-68; G01N033-567; A61K007-06
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 27 OF 135 USPATFULL on STN
 AN 2002:181561 USPATFULL
 TI Process for in vitro selection of high methol producing genotypes
 IN Khanuja, Suman Preet Singh, Lucknow, INDIA
 Shasany, Ajit Kumar, Lucknow, INDIA
 Dhawan, Sunita, Lucknow, INDIA
 Darokar, Mahendra Pandurang, Lucknow, INDIA
 Kumar, Tiruppadiripuliyur Ranganathan Santha, Lucknow, INDIA
 Saikia, Dharmendra, Lucknow, INDIA
 Naqui, Arif Ali, Lucknow, INDIA
 Kumar, Sushil, Lucknow, INDIA
 PA Council of Scientific&Industrial Reaearch, New Delhi, INDIA (non-U.S.
 corporation)
 PI US 6423541 B1 20020723
 AI US 2000-531768 20000321 (9)
 DT Utility
 FS GRANTED
 LN.CNT 741
 INCL INCLM: 435/420.000
 INCLS: 435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
 NCL NCLM: 435/420.000
 NCLS: 435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
 IC [7]
 ICM: C12N005-00
 EXF 435/410; 435/420; 435/421; 435/430; 435/430.1; 435/431
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 28 OF 135 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
 AN 2002-547451 [58] WPIDS
 DNC C2002-155181
 TI Treatment or prophylaxis of a subject having a disorder characterized by
 abnormal interaction of Grb7 and a Grb7 ligand, involves administering to
 a non-phosphorylated peptide to a subject in need of the treatment.

DC B04 D16
 IN Krag, D N; OLIGINO, L; PERO, S C
 PA (UYVE-N) UNIV VERMONT & STATE AGRIC COLLEGE; (Krag-I) Krag D N; (OLIG-I)
 OLIGINO L; (PERO-I) PERO S C
 CYC 23
 PI WO 2002036142 A2 20020510 (200258)* EN 95p A61K038-00
 RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
 W: AU CA JP
 AU 2002020265 A 20020515 (200258) A61K038-00
 US 2003105000 A1 20030605 (200339) A61K038-17
 ADT WO 2002036142 A2 WO 2001-US47400 20011105; AU 2002020265 A AU 2002-20265
 20011105; US 2003105000 A1 Provisional US 2000-245755P 20001103, US
 2001-13815 20011105
 FDT AU 2002020265 A Based on WO 2002036142
 PRAI US 2000-245755P 20001103; US 2001-13815 20011105
 IC ICM A61K038-00; A61K038-17

L6 ANSWER 29 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 14
 AN 2002:492206 BIOSIS
 DN PREV200200492206
 TI Association of Grb7 with phosphoinositides and its role in the regulation
 of cell migration.
 AU Shen, Tang-Long; Han, Dong Cho; Guan, Jun-Lin [Reprint author]
 CS Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
 USA
 jg19@cornell.edu
 SO Journal of Biological Chemistry, (August 9, 2002) Vol. 277, No. 32, pp.
 29069-29077. print.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 ED Entered STN: 18 Sep 2002
 Last Updated on STN: 18 Sep 2002

L6 ANSWER 30 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 15
 AN 2002:292126 BIOSIS
 DN PREV200200292126
 TI Identification of novel non-phosphorylated ligands, which bind selectively
 to the SH2 domain of Grb7.
 AU Pero, Stephanie C.; Oligino, Lyn; Daly, Roger J.; Soden, Amy L.; Liu,
 Chen; Roller, Peter P.; Li, Peng; Krag, David N. [Reprint author]
 CS Department of Surgery, University of Vermont School of Medicine, Given
 Medical Building, Rm. E309, Burlington, VT, 05405, USA
 David.Krag@uvm.edu
 SO Journal of Biological Chemistry, (April 5, 2002) Vol. 277, No. 14, pp.
 11918-11926. print.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 ED Entered STN: 15 May 2002
 Last Updated on STN: 15 May 2002

L6 ANSWER 31 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2002:875636 CAPLUS
 DN 138:151170
 TI Comparative analysis of mutation frequency of coding and non coding short
 mononucleotide repeats in mismatch repair deficient colorectal cancers
 AU Duval, Alex; Reperant, Maryline; Hamelin, Richard
 CS INSERM U434, CEPH, Paris, Fr.
 SO Oncogene (2002), 21(52), 8062-8066
 CODEN: ONCNE5; ISSN: 0950-9232
 PB Nature Publishing Group
 DT Journal
 LA English
 RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 32 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 16
 AN 2002:529717 BIOSIS
 DN PREV200200529717
 TI The adapter protein ZIP binds ***Grb14*** and regulates its inhibitory
 action on insulin signaling by recruiting protein kinase Czeta.
 AU Cariou, Bertrand; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly,

Edith; Bereziat, Veronique; Vasseur-Cognet, Mireille; Girard, Jean;
Burnol, Anne-Francoise [Reprint author]
CS Departement d'Endocrinologie, Institut Cochin, CNRS-INSERM-Universite Rene
Descartes, 24 Rue du Faubourg Saint-Jacques, 75674, Paris, France
burnol@cochin.inserm.fr
SO Molecular and Cellular Biology, (October, 2002) Vol. 22, No. 20, pp.
6959-6970. print.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
LA English
ED Entered STN: 16 Oct 2002
Last Updated on STN: 16 Oct 2002

L6 ANSWER 33 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 17
AN 2002:207358 BIOSIS
DN PREV200200207358
TI Inhibition of insulin receptor catalytic activity by the molecular adapter
Grb14
AU Bereziat, Veronique; Kasus-Jacobi, Anne; Perdereau, Dominique; Cariou,
Bertrand; Girard, Jean; Burnol, Anne-Francoise [Reprint author]
CS Endocrinologie et Metabolisme, CNRS UPR 1524, Institut Cochin de Genetique
Moleculaire, 24 rue du Faubourg Saint-Jacques, 75674, Paris Cedex, 14,
France
burnol@cochin.inserm.fr
SO Journal of Biological Chemistry, (February 15, 2002) Vol. 277, No. 7, pp.
4845-4852. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 20 Mar 2002
Last Updated on STN: 20 Mar 2002

L6 ANSWER 34 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:3572 CAPLUS
DN 138:382650
TI Ontogeny and the possible function of a novel epidermal growth factor-like
repeat domain-containing protein, NELL2, in the rat brain
AU Kim, Hyun; Ha, Chang Man; Choi, Jungil; Choi, Eun Jung; Jeon, Jongrye;
Kim, Changmee; Park, Sang Kyu; Kang, Sang Soo; Kim, Kyungjin; Lee, Byung
Ju
CS Department of Anatomy, Brain Korea 21 Biomedical Sciences, Korea
University College of Medicine, Seoul, S. Korea
SO Journal of Neurochemistry (2002), 83(6), 1389-1400
CODEN: JONRA9; ISSN: 0022-3042
PB Blackwell Science Ltd.
DT Journal
LA English
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 35 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:396091 BIOSIS
DN PREV200200396091
TI Gene expression profiling of endometrial carcinomas: Identification of
molecular biomarkers.
AU Yap, Oi Wah Stephanie [Reprint author]; Zhu, Shirley [Reprint author]; van
de Rijn, Matt [Reprint author]; Longacre, Teri [Reprint author]; Teng,
Nelson [Reprint author]; Husain, Amreen [Reprint author]
CS Stanford University Medical Center, Stanford, CA, USA
SO Proceedings of the American Association for Cancer Research Annual
Meeting, (March, 2002) Vol. 43, pp. 746. print.
Meeting Info.: 93rd Annual Meeting of the American Association for Cancer
Research. San Francisco, California, USA. April 06-10, 2002.
ISSN: 0197-016X.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 24 Jul 2002
Last Updated on STN: 24 Jul 2002

L6 ANSWER 36 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2002:207936 SCISEARCH
GA The Genuine Article (R) Number: 524UV
TI Comparison of gene expression in old versus young rat hippocampus by cDNA
array

AU Cho K S; Choi J G; Ha C M; Son Y J; Choi W S; Lee B J (Reprint)
 CS Univ Ulsan, Dept Biol Sci, Ulsan 680749, South Korea (Reprint); Gyeongsang
 Natl Univ, Coll Med, Dept Anat, Chinju 660280, South Korea
 CYA South Korea
 SO NEUROREPORT, (4 MAR 2002) Vol. 13, No. 3, pp. 285-289.
 Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA
 19106-3621 USA.
 ISSN: 0959-4965.
 DT Article; Journal
 LA English
 REC Reference Count: 26
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L6 ANSWER 37 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 18
 AN 2003:124261 BIOSIS
 DN PREV200300124261
 TI Assignment of backbone 1H, 13C, and 15N resonances of the SH2 domain of
 human ***Grb14***
 AU Scharf, Paul J.; Lyons, Barbara A. [Reprint Author]
 CS Department of Biochemistry, College of Medicine, University of Vermont,
 Burlington, VT, 05405, USA
 blyons@zoo.uvm.edu
 SO Journal of Biomolecular NMR, (November 2002) Vol. 24, No. 3, pp. 275-276.
 print.
 ISSN: 0925-2738 (ISSN print).
 DT Article
 LA English
 ED Entered STN: 5 Mar 2003
 Last Updated on STN: 5 Mar 2003

L6 ANSWER 38 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
 AN 2002:524711 SCISEARCH
 GA The Genuine Article (R) Number: 557XP
 TI The atypical PKC-Interacting protein ZIP binds ***Grb14*** and
 potentiates its inhibitory action on insulin signaling
 AU Cariou B (Reprint); Perdereau D; Cailliau K; Browaeys-Poly E; Bereziat V;
 Girard J; Burnol A F
 SO DIABETES, (JUN 2002) Vol. 51, Supp. [2], pp. A56-A56. MA 228.
 Publisher: AMER DIABETES ASSOC, 1660 DUKE ST, ALEXANDRIA, VA 22314 USA.
 ISSN: 0012-1797.
 DT Conference; Journal
 LA English
 REC Reference Count: 0

L6 ANSWER 39 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2003:155451 BIOSIS
 DN PREV200300155451
 TI Proteomic Study on the Retinas of RD, RDS and C3B Mice as well as
 Reconfirming of the Differentially Expressed Proteins by Using RT-PCT.
 AU Li, D. [Reprint Author]; Zhang, Q. J.
 CS Ocular Genetics and Molec Bio, Zhonghsan Ophthalmic Ctr, GuanZhou, China
 SO ARVO Annual Meeting Abstract Search and Program Planner, (2002) Vol. 2002,
 pp. Abstract No. 3629. cd-rom.
 Meeting Info.: Annual Meeting of the Association For Research in Vision
 and Ophthalmology. Fort Lauderdale, Florida, USA. May 05-10, 2002.
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 26 Mar 2003
 Last Updated on STN: 26 Mar 2003

L6 ANSWER 40 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:798473 CAPLUS
 DN 135:340282
 TI Nucleic acid sequences associated with baldness and uses in detecting the
 likelihood of baldness and for gene therapy
 IN Pritchard, David; Burmer, Glenna; Brown, Joseph; Demas, Vasiliki
 PA Lifespan Biosciences, Inc., USA
 SO PCT Int. Appl., 87 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	-----	-----	-----	-----

PI WO 2001081628 A1 20011101 WO 2001-US12184 20010413
 WO 2001081628 C2 20021227
 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
 CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
 RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
 VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 RW: GH, GU, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
 BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002177566 A1 20021128 US 2001-825096 20010402
 PRAI US 2000-199745P P 20000425

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 41 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 19
 AN 2001:390236 BIOSIS
 DN PREV200100390236
 TI Identification of a novel human tankyrase through its interaction with the
 adaptor protein ****Grb14****
 AU Lyons, Ruth J.; Deane, Roisin; Lynch, Danielle K.; Ye, Zheng-Sheng
 Jeffrey; Sanderson, Georgina M.; Eyre, Helen J.; Sutherland, Grant R.;
 Daly, Roger J. [Reprint author]
 CS Cancer Research Program, Garvan Institute of Medical Research, St.
 Vincent's Hospital, Sydney, NSW, 2010, Australia
 r.daly@garvan.org.au
 SO Journal of Biological Chemistry, (May 18, 2001) Vol. 276, No. 20, pp.
 17172-17180. print.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 OS Genbank-AF329696
 ED Entered STN: 15 Aug 2001
 Last Updated on STN: 23 Feb 2002

L6 ANSWER 42 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 20
 AN 2001:514026 BIOSIS
 DN PREV200100514026
 TI The Grb7 family proteins: Structure, interactions with other signaling
 molecules and potential cellular functions.
 AU Han, Dong Cho; Shen, Tang-Long; Guan, Jun-Lin [Reprint author]
 CS Cancer Biology Laboratories, Department of Molecular Medicine, Cornell
 University, Ithaca, NY, 14853, USA
 jgl19@cornell.edu
 SO Oncogene, (1 October, 2001) Vol. 20, No. 44, pp. 6315-6321. print.
 CODEN: ONCNES. ISSN: 0950-9232.
 DT Article
 General Review; (Literature Review)
 LA English
 ED Entered STN: 7 Nov 2001
 Last Updated on STN: 23 Feb 2002

L6 ANSWER 43 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:634713 CAPLUS
 DN 135:342315
 TI Extensive characterization of genetic alterations in a series of human
 colorectal cancer cell lines
 AU Gayet, Jacqueline; Zhou, Xiao-Ping; Duval, Alex; Rolland, Sandra; Hoang,
 Jean-Marc; Cottu, Paul; Hamelin, Richard
 CS INSERM U434 - CEPH, Paris, 75010, Fr.
 SO Oncogene (2001), 20(36), 5025-5032
 CODEN: ONCNES; ISSN: 0950-9232
 PB Nature Publishing Group
 DT Journal
 LA English
 RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 44 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 21
 AN 2001:170169 CAPLUS
 DN 135:270832
 TI Evolution of instability at coding and non-coding repeat sequences in
 human MSI-H colorectal cancers

AU Duval, Alex; Rolland, Sandra; Compoint, Aureole; Tubacher, Emmanuel;
Iacopetta, Barry; Thomas, Gilles; Hamelin, Richard
CS INSERM U434, CEPH, Paris, 75010, Fr.
SO Human Molecular Genetics (2001), 10(5), 513-518
CODEN: HMGE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 45 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 22
AN 2001:209006 BIOSIS
DN PREV200100209006
TI The BPS domain of Grb10 inhibits the catalytic activity of the insulin and
IGF1 receptors.
AU Stein, Evan G.; Gustafson, Thomas A.; Hubbard, Stevan R. [Reprint author]
CS Department of Pharmacology, Skirball Institute of Biomolecular Medicine,
New York University School of Medicine, 540 First Avenue, New York, NY,
10016, USA
hubbard@tallis.med.nyu.edu
SO FEBS Letters, (30 March, 2001) vol. 493, No. 2-3, pp. 106-111. print.
CODEN: FEBLAL. ISSN: 0014-5793.
DT Article
LA English
ED Entered STN: 2 May 2001
Last Updated on STN: 18 Feb 2002

L6 ANSWER 46 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:69396 BIOSIS
DN PREV200200069396
TI Inhibition of insulin receptors tyrosine kinase activity by the molecular
adapter ****Grb14****
AU Bereziat, V. [Reprint author]; Kasus-Jacobi, A. [Reprint author];
Perdereau, D. [Reprint author]; Girard, J. [Reprint author]; Burnol, A.-F.
[Reprint author]
CS CNRS UPR1524, ICGM, 9 rue Jules Hetzel, 92190, Meudon, France
SO Biochemical Society Transactions, (2001) vol. 29, No. 3, pp. A69. print.
Meeting Info.: 673rd Bristol Meeting of the Biochemical Society. Bristol,
London, UK. April 10-12, 2000. Biochemical Society.
CODEN: BCSTB5. ISSN: 0300-5127.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 16 Jan 2002
Last Updated on STN: 25 Feb 2002

L6 ANSWER 47 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 23
AN 2001:131521 CAPLUS
DN 134:202914
TI Human growth factor receptor bound 14 binds the activated insulin receptor
and alters the insulin-stimulated tyrosine phosphorylation levels of
multiple proteins
AU Hemming, Richard; Agatep, Ronald; Badiani, Ketan; Wyant, Kerrie; Arthur,
Gilbert; Gietz, R. Daniel; Triggs-Raine, Barbara
CS Department of Biochemistry & Medical Genetics, University of Manitoba,
Winnipeg, MB, R3E 0W3, Can.
SO Biochemistry and Cell Biology (2001), 79(1), 21-32
CODEN: BCBIEQ; ISSN: 0829-8211
PB National Research Council of Canada
DT Journal
LA English
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 48 OF 135 DISSABS COPYRIGHT (C) 2004 Proquest Information and
Learning Company; All Rights Reserved on STN
AN 2001:8470 DISSABS order Number: AAINQ49934
TI Identification and characterization of downstream signaling partners of
the endothelial cell-specific receptor tyrosine kinase, Tek/Tie-2
AU Jones, Nina [Ph.D.]; Dumont, Daniel J. [adviser]
CS University of Toronto (Canada) (0779)
SO Dissertation Abstracts International, (2000) vol. 61, No. 6B, p. 2900.
order No.: AAINQ49934. 175 pages.
ISBN: 0-612-49934-0.

DT Dissertation
FS DAI
LA English

L6 ANSWER 49 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company; All Rights Reserved on STN
AN 2001:38658 DISSABS Order Number: AAIMQ51679
TI The insulin signaling pathway: Evidence that Tax1bp1/Txbp151 is a dimeric human ***Grb14*** interacting protein
AU Agatep, Ronald [M.Sc.]; Gietz, R. D. [adviser]
CS The University of Manitoba (Canada) (0303)
SO Masters Abstracts International, (2000) Vol. 39, No. 1, p. 151. Order No.: AAIMQ51679. 143 pages.
ISBN: 0-612-51679-2.
DT Dissertation
FS MAI
LA English

L6 ANSWER 50 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 24
AN 2000:666978 CAPLUS
DN 133:247252
TI ***Grb14*** proteins for screening compounds capable of modulating insulin receptor tyrosine kinase activity
IN Burnol, Anne-Francoise; Perdereau, Dominique; Kasus-Jacobi, Anne; Bereziat, Veronique; Girard, Jean
PA Centre National De La Recherche Scientifique-CNRS, Fr.
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000055634	A1	20000921	WO 2000-FR613	20000314
	W: AU, CA, JP, NZ, US, ZA				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	FR 2790956	A1	20000922	FR 1999-3159	19990315
	FR 2790956	B1	20030523		
	EP 1161687	A1	20011212	EP 2000-910938	20000314
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	NZ 514668	A	20030829	NZ 2000-514668	20000314
	ZA 2001007546	A	20020829	ZA 2001-7546	20010913
PRAI	FR 1999-3159	A	19990315		
	WO 2000-FR613	W	20000314		
RE.CNT	10	THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT			

L6 ANSWER 51 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 25
AN 2000:345087 BIOSIS
DN PREV200000345087
TI Association of fibroblast growth factor receptor 1 with the adaptor protein ***Grb14***. Characterization of a new receptor binding partner.
AU Reilly, John F.; Mickey, Gregory; Maher, Pamela A. [Reprint author]
CS Dept. of Cell Biology, The Scripps Research Institute, 10550 N. Torrey Pines Rd., CAL-3, La Jolla, CA, 92037, USA
SO Journal of Biological Chemistry, (March 17, 2000) Vol. 275, No. 11, pp. 7771-7778. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 16 Aug 2000
Last Updated on STN: 7 Jan 2002

L6 ANSWER 52 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 26
AN 2000:224729 BIOSIS
DN PREV200000224729
TI Evidence for an interaction between the insulin receptor and Grb7. A role for two of its binding domains, PIR and SH2.
AU Kasus-Jacobi, Anne; Bereziat, Veronique; Perdereau, Dominique; Girard, Jean; Burnol, Anne-Francoise [Reprint author]
CS Endocrinologie Metabolisme et Developpement, CNRS, UPR 1524, 9 Rue Jules

SO Hetzel, 92190, Meudon, France
 Oncogene, (April 13, 2000) Vol. 19, No. 16, pp. 2052-2059. print.
 CODEN: ONCNES. ISSN: 0950-9232.
 DT Article
 LA English
 ED Entered STN: 31 May 2000
 Last Updated on STN: 5 Jan 2002

L6 ANSWER 53 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 27
 AN 2000:334281 BIOSIS
 DN PREV200000334281
 TI Grb10 proteins in insulin-like growth factor and insulin receptor
 signaling (Review).
 AU Morrione, Andrea [Reprint author]
 CS Kimmel Cancer Center, Thomas Jefferson University, 233 South 10th Street,
 606 Bluemle Life Sciences Building, Philadelphia, PA, 19107-5541, USA
 SO International Journal of Molecular Medicine, (Feb., 2000) Vol. 5, No. 2,
 pp. 151-154. print.
 ISSN: 1107-3756.
 DT Article
 General Review; (Literature Review)
 LA English
 ED Entered STN: 10 Aug 2000
 Last Updated on STN: 7 Jan 2002

L6 ANSWER 54 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1999:223032 CAPLUS
 DN 130:247888
 TI Potential effector protein for the Grb7 family of signaling proteins
 IN Daly, Roger John; Sutherland, Robert Lyndsay
 PA Garvan Institute of Medical Research, Australia
 SO PCT Int. Appl., 26 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9915647	A1	19990401	WO 1998-AU795	19980923
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2303760	AA	19990401	CA 1998-2303760	19980923
AU 9892458	A1	19990412	AU 1998-92458	19980923
AU 727305	B2	20001207		
EP 1017802	A1	20000712	EP 1998-944896	19980923
R: CH, DE, FR, GB, IT, LI, SE				
JP 2001517435	T2	20011009	JP 2000-512939	19980923
US 2002037582	A1	20020328	US 2000-509196	20000323
PRAI AU 1997-9388	A	19970923		
WO 1998-AU795	W	19980923		

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 55 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 28
 AN 2000:433637 BIOSIS
 DN PREV200000433637
 TI Identification of Tek/Tie2 binding partners. Binding to a multifunctional
 docking site mediates cell survival and migration.
 AU Jones, Nina; Master, Zubin; Jones, Jamie; Bouchard, Denis; Gunji, Yuji;
 Sasaki, Hiroki; Daly, Roger; Alitalo, Kari; Dumont, Daniel J. [Reprint
 author]
 CS Sunnybrook and Women's College Health Sciences Centre, 2075 Bayview Ave.,
 Research Bldg., S-227, Toronto, ON, M4N 3M5, Canada
 SO Journal of Biological Chemistry, (Oct. 22, 1999) Vol. 274, No. 43, pp.
 30896-30905. print.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English

ED Entered STN: 11 Oct 2000
Last Updated on STN: 10 Jan 2002

L6 ANSWER 56 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 29
AN 1999:288188 BIOSIS
DN PREV199900288188
TI Sequence analysis identifies a Ras-associating (RA)-like domain in the
N-termini of band 4.1/JEF domains and in the Grb7/10/14 adapter family.
AU Wojcik, Jerome; Girault, Jean-Antoine; Labesse, Gilles; Chomilier,
Jacques; Mornon, Jean-Paul; Callebaut, Isabelle [Reprint author]
CS systemes moleculaires and Biologie structurale, LMCP, CNRS UMR 7590,
Universites Paris 6 et Paris 7, 4 place Jussieu, 75252, Paris Cedex 05,
France
SO Biochemical and Biophysical Research Communications, (May 27, 1999) Vol.
259, No. 1, pp. 113-120. print.
CODEN: BBRCA9. ISSN: 0006-291X.
DT Article
LA English
ED Entered STN: 5 Aug 1999
Last Updated on STN: 5 Aug 1999

L6 ANSWER 57 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 30
AN 1998:491148 BIOSIS
DN PREV199800491148
TI Identification of the rat adapter ***Grb14*** as an inhibitor of
insulin actions.
AU Kasus-Jacobi, Anne; Perdereau, Dominique; Auzan, Colette; Clauser, Eric;
Van Obberghen, Emmanuel; Mauvais-Jarvis, Franck; Girard, Jean; Burnol,
Anne-Francoise [Reprint author]
CS Endocrinologie Metabolisme et Developpement, CNRS, UPR 1524, 9 rue Jules
Hetzel, 92190 Meudon, France
SO Journal of Biological Chemistry, (Oct. 2, 1998) Vol. 273, No. 40, pp.
26026-26035. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS Genbank-AF076619
ED Entered STN: 18 Nov 1998
Last Updated on STN: 18 Nov 1998

L6 ANSWER 58 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 31
AN 1998:251777 BIOSIS
DN PREV199800251777
TI Interaction of the Grb10 adapter protein with the Raf1 and MEK1 kinases.
AU Nantel, Andre [Reprint author]; Mohammad-Ali, Khosro; Sherk, Jennifer;
Posner, Barry I.; Thomas, David Y.
CS Eukaryotic Genet. Group, Biotechnol. Res. Inst., Natl. Res. Council, 6100
Royalmount, Montreal, PQ H4P 2R2, Canada
SO Journal of Biological Chemistry, (April 24, 1998) Vol. 273, No. 17, pp.
10475-10484. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 9 Jun 1998
Last Updated on STN: 12 Aug 1998

L6 ANSWER 59 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 32
AN 1998:225785 BIOSIS
DN PREV199800225785
TI Grb10 interacts differentially with the insulin receptor, insulin-like
growth factor I receptor, and epidermal growth factor receptor via the
Grb10 src homology 2 (SH2) domain and a second novel domain located
between the Pleckstrin homology and SH2 domains.
AU He, Weimin; Rose, David W.; Olefsky, Jerrold M.; Gustafson, Thomas A.
[Reprint author]
CS Metabolex Inc., 3876 Bay Cent. Pl., Hayward, CA 94545, USA
SO Journal of Biological Chemistry, (March 20, 1998) Vol. 273, No. 12, pp.
6860-6867. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 20 May 1998

Last Updated on STN: 20 May 1998

L6 ANSWER 60 OF 135 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 1998:907280 SCISEARCH
GA The Genuine Article (R) Number: 137GQ
TI A novel FGF signaling pathway u ***Grb14*** binds to FGF receptor 1.
AU Reilly J F (Reprint); Mickey G; Maher P A
CS SCRIPPS RES INST, DEPT CELL BIOL, LA JOLLA, CA 92037
CYA USA
SO MOLECULAR BIOLOGY OF THE CELL, (NOV 1998) Vol. 9, Supp. [S], pp.
1365-1365.
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE,
BETHESDA, MD 20814.
ISSN: 1059-1524.
DT Conference; Journal
FS LIFE
LA English
REC Reference Count: 0

L6 ANSWER 61 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:443196 BIOSIS
DN PREV199800443196
TI The Grb7 family of signalling proteins.
AU Daly, Roger J. [Reprint author]
CS Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
NSW 2010, Australia
SO Cellular Signalling, (Oct., 1998) Vol. 10, No. 9, pp. 613-618. print.
CODEN: CESIEY. ISSN: 0898-6568.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 21 Oct 1998
Last Updated on STN: 21 Oct 1998

L6 ANSWER 62 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:16001 BIOSIS
DN PREV199900016001
TI A novel FGF signaling pathway u ***GRB14*** binds to FGF receptor 1.
AU Reilly, John F.; Mickey, Gregory; Maher, Pamela A.
CS Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
SO Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No. SUPPL., pp. 236A.
print.
Meeting Info.: 38th Annual Meeting of the American Society for Cell
Biology. San Francisco, California, USA. December 12-16, 1998. American
Society for Cell Biology.
CODEN: MBCEEV. ISSN: 1059-1524.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999

L6 ANSWER 63 OF 135 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
Learning Company; All Rights Reserved on STN
AN 97:70470 DISSABS Order Number: AAR0598267 (not available for sale by
UMI)
TI ERBB RECEPTOR SIGNALLING IN HUMAN BREAST CANCER (TYROSINE KINASES)
AU JAMES, PETER WARWICK [PH.D.]
CS UNIVERSITY OF NEW SOUTH WALES (AUSTRALIA) (0423)
SO Dissertation Abstracts International, (1997) Vol. 58, No. 6B, p. 2970.
Order No.: AAR0598267 (not available for sale by UMI).
DT Dissertation
FS DAI
LA English
ED Entered STN: 19971104
Last Updated on STN: 19971104

L6 ANSWER 64 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 33
AN 1998:28109 BIOSIS
DN PREV199800028109
TI Cloning, chromosome localization, expression, and characterization of an
Src homology 2 and pleckstrin homology domain-containing insulin receptor
binding protein hgrb10gamma.
AU Dong, Lily Q.; Du, Hongyan; Porter, Sarah G.; Kolakowski, Lee F., Jr.;
Lee, Adrian V.; Mandarino, J.; Fan, Jianbing; Yee, Douglas; Liu, Feng

[Reprint author]
 CS Dep. Pharmacol., Univ. Texas Health Sci. Cent., 7703 Floyd Curl Dr., San
 Antonio, TX 78284-7764, USA
 SO Journal of Biological Chemistry, (Nov. 14, 1997) Vol. 272, No. 46, pp.
 29104-29112. print.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 OS Genbank-AF001534
 ED Entered STN: 14 Jan 1998
 Last Updated on STN: 14 Jan 1998

L6 ANSWER 65 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 34
 AN 1997:221295 BIOSIS
 DN PREV199799513011
 TI Structural determinants of the interaction between the erbB2 receptor and
 the Src homology 2 domain of Grb7.
 AU Janes, Peter W.; Lackmann, Martin; Church, W. Bret; Sanderson, Georgina
 M.; Sutherland, Robert L.; Daly, Roger J. [Reprint author]
 CS Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
 NSW 2010, Australia
 SO Journal of Biological Chemistry, (1997) Vol. 272, No. 13, pp. 8490-8497.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 ED Entered STN: 22 May 1997
 Last Updated on STN: 22 May 1997

L6 ANSWER 66 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 35
 AN 1997:110178 BIOSIS
 DN PREV199799409381
 TI Human GRB-IR-beta/GRB10: splice variants of an insulin and growth factor
 receptor-binding protein with PH and SH2 domains.
 AU Frantz, J. Daniel; Giorgetti-Peraldi, Sophie; Ottinger, Elizabeth A.;
 Shoelson, Steven E. [Reprint author]
 CS Joslin Diabetes Cent., One Joslin Place, Boston, MA 02215, USA
 SO Journal of Biological Chemistry, (1997) Vol. 272, No. 5, pp. 2659-2667.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 ED Entered STN: 10 Mar 1997
 Last Updated on STN: 10 Mar 1997

L6 ANSWER 67 OF 135 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 36
 AN 1997:26254 CAPLUS
 DN 126:43162
 TI GDU: a new target for the erbB family of protein tyrosine kinases and a
 cDNA encoding it
 IN Daly, Roger John; Sutherland, Robert Lyndsay
 PA Garvan Institute of Medical Research, Australia; Daly, Roger John;
 Sutherland, Robert Lyndsay
 SO PCT Int. Appl., 15 pp.
 CODEN: PIXXD2

DT Patent
 LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9634951	A1	19961107	WO 1996-AU258	19960502
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
	CA 2220016	AA	19961107	CA 1996-2220016	19960502
	AU 9654904	A1	19961121	AU 1996-54904	19960502
	AU 701733	B2	19990204		
	EP 840786	A1	19980513	EP 1996-911844	19960502
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 11505415	T2	19990521	JP 1996-532859	19960502
	US 2002086328	A1	20020704	US 1998-945771	19980422
	US 6465623	B2	20021015		

	US 2003044834	A1	20030306	US 2002-242332	20020911
	US 2003129639	A1	20030710	US 2002-323001	20021218
PRAI	AU 1995-2742	A	19950502		
	WO 1996-AU258	W	19960502		
	US 1998-945771	A3	19980422		
	US 2002-242332	A3	20020911		

L6 ANSWER 68 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 37
 AN 1996:484539 BIOSIS
 DN PREV199699199795
 TI Cloning and characterization of ***GRB14*** , a novel member of the
 GRB7 gene family.
 AU Daly, Roger J. [Reprint author]; Sanderson, Georgina M.; Janes, Peter W.;
 Sutherland, Robert L.
 CS Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
 NSW 2010, Australia
 SO Journal of Biological Chemistry, (1996) Vol. 271, No. 21, pp. 12502-12510.
 CODEN: JBCHA3. ISSN: 0021-9258.
 DT Article
 LA English
 OS EMBL-L76687; Genbank-L76687
 ED Entered STN: 24 Oct 1996
 Last Updated on STN: 10 Dec 1996

L6 ANSWER 69 OF 135 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 DUPLICATE 38
 AN 1996:438181 BIOSIS
 DN PREV199699151787
 TI Assignment of the human ***GRB14*** gene to chromosome 2q22-q24 by
 fluorescence in situ hybridization.
 AU Baker, Elizabeth; Sutherland, Grant R.; Sutherland, Robert L.; Daly, Roger
 J. [Reprint author]
 CS Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
 NSW 2010, Australia
 SO Genomics, (1996) Vol. 36, No. 1, pp. 218-220.
 CODEN: GNMCEP. ISSN: 0888-7543.
 DT Article
 LA English
 OS EMBL-L76687; Genbank-L76687
 ED Entered STN: 26 Sep 1996
 Last Updated on STN: 5 Nov 1996

L6 ANSWER 70 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN AAW07871 Protein DGENE
 TI A new signalling protein designated GDU related to erbB receptor targets
 - also DNA encoding it, probes, and monoclonal antibodies for detection
 and treatment of breast and prostate cancer
 IN Daly R J; Sutherland R L
 PA (GARV-N) GARVAN INST MEDICAL RES.
 PI WO 9634951 A1 19961107 17p
 AI WO 1996-AU258 19960502
 PRAI AU 1995-2742 19950502
 DT Patent
 LA English
 OS 1996-506156 [50]
 CR N-PSDB: AAT44581
 DESC GDU (or ***Grb14***), a signalling protein.

L6 ANSWER 71 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN AAX25366 cDNA DGENE
 TI New candidate effector for the Grb7 family of signaling proteins, and
 specific antibody, useful for detection and treatment of cancer
 IN Daly R J; Sutherland R L
 PA (GARV-N) GARVAN INST MEDICAL RES.
 PI WO 9915647 A1 19990401 24p
 AI WO 1998-AU795 19980923
 PRAI AU 1997-9388 19970923
 DT Patent
 LA English
 OS 1999-254707 [21]
 CR P-PSDB: AAY05734
 DESC Human Grb7 effector 2.2412 cDNA.

L6 ANSWER 72 OF 135 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
 AN AAT44581 DNA DGENE

TI A new signalling protein designated GDU related to erbB receptor targets
 - also DNA encoding it, probes, and monoclonal antibodies for detection
 and treatment of breast and prostate cancer
 IN Daly R J; Sutherland R L
 PA (GARV-N) GARVAN INST MEDICAL RES.
 PI WO 9634951 A1 19961107 17p
 AI WO 1996-AU258 19960502
 PRAI AU 1995-2742 19950502
 DT Patent
 LA English
 OS 1996-506156 [50]
 CR P-PSDB: AAW07871
 DESC GDU (or ***Grb14***), a signalling protein.

L6 ANSWER 73 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419444 GenBank (R)
 GenBank ACC. NO. (GBN): AY419444
 GenBank VERSION (VER): AY419444.1 GI:39775401
 CAS REGISTRY NO. (RN): 629064-36-4
 SEQUENCE LENGTH (SQL): 1361
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Genome Survey Sequence
 DATE (DATE): 17 Dec 2003
 DEFINITION (DEF): Mus musculus ***GRB14*** gene, VIRTUAL TRANSCRIPT,
 partial sequence, genomic survey sequence.
 GSS
 KEYWORDS (ST):
 SOURCE: Mus musculus (house mouse)
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

COMMENT:

These sequences were made by sequencing genomic exons and ordering
 them based on alignment.

REFERENCE: 1 (bases 1 to 1361)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse
 orthologous gene trios
 JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
 REFERENCE: 2 (bases 1 to 1361)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude
 Drive, Rockville, MD 20850, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1361	/organism="Mus musculus" /mol-type="genomic DNA" /db-xref="taxon:10090"
gene	<1..>1361	/gene="GRB14" /locus-tag="HCM6892"

SEQUENCE (SEQ):

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1 atgagtctga gtgcaagaag agtcaccctg cctgcgataa caccaatagt tctacagaag
61 aggnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
121 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
181 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aaagaaccgt agaggaccac
241 gagctgccaa ctgaagtgtg gtctcactgg ggagtggaaag aagacaataa gctgtatctt
301 agaaagaatt atgccaaata tgaatttttt aagaacccaa tgnnnnnnnn nnnnnnnnnn
361 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnngtg
421 tttttaagct ccagcacgta tcctgaaatc catggcttct tacatgcaaa ggaacaggga
481 aagaagtctt ggaaaaaagc ttactttttt ctcagaagat ctggcctata ttttctact
541 aaaggcacat ccaaggaacc acggcatttg cagcttttca gtgaattcag cactagtcac
601 gtttatatgt cactggcagg aaaaaaaa cacggagcgc caactcccta tggattctgc
661 ttaaacctaa caaagcagga gggcccccgg acctgaaaat gctctgtgca gaagaagagc
721 agagcaggac gtgctgggtg accgccatcc gactgctgaa gnnnnnnnnn nnnnnnnnnn
781 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
  
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841 nnagaagcgt atcagagaat tccctagtag caatggactt ctcagggtgag aagagcagag
901 tcatagacaa cccactgaa gcgctttcgg ttgctgttga ggaaggcctc gcgtgggagga
961 aaaaaggctg tttacgcctg gggaaatcac gaagcccccag tgccccctcc cagagctctg
1021 ctgtgaacat ggctctccat cgggtcccaac catggtttca ccacagaatt tccagagatg
1081 aggtcagcg gctgatcatt cggcaggggc ctgtggatgg agttttcttg gtacgggata
1141 gtcagagtaa ccccagaact tttgtactgt caatgagtca tggacaaaag ataaaacact
1201 atcaaattat acccgtagaa gatgatgggt agctgtttcca tactctggat gatggccata
1261 cgaagttcac agacctcatc cagctgggtg agttctacca gctcaacagg ggggtccttc
1321 ctgcaagct gaagcattac tgtgctagga tggctgttta g

L6 ANSWER 74 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419443 GenBank (R)
GenBank ACC. NO. (GBN): AY419443
GenBank VERSION (VER): AY419443.1 GI:39775400
CAS REGISTRY NO. (RN): 629064-35-3
SEQUENCE LENGTH (SQL): 1362
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Genome Survey Sequence
DATE (DATE): 17 Dec 2003
DEFINITION (DEF): Pan troglodytes ***GRB14*** gene, VIRTUAL
TRANSCRIPT, partial sequence, genomic survey sequence.
KEYWORDS (ST): GSS
SOURCE: Pan troglodytes (chimpanzee)
ORGANISM (ORGN): Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Pan

COMMENT:
These sequences were made by sequencing genomic exons and ordering
them based on alignment.

REFERENCE: 1 (bases 1 to 1362)
AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse
orthologous gene trios
JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
REFERENCE: 2 (bases 1 to 1362)
AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude
Drive, Rockville, MD 20850, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1362	/organism="Pan troglodytes" /mol-type="genomic DNA" /db-xref="taxon:9598"
gene	<1..>1362	/gene="GRB14" /locus-tag="HCM6892"

SEQUENCE (SEQ):

1 atgagtttga gtgcaagaag agtcactctg cctgcaataa cgccaataat tctacagaaa
61 aggnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
121 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
181 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnaat agaagaccac
241 gaactgggtga ttgaagtgtc atccaactgg gggatagaag aagaaaacaa actannnnnn
301 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
361 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnatg
421 ttctgagtt caagcacata tcttgaaatt catggtttct tacatgcgaa agaacaggga
481 aagaagttctt ggaaaaaaat ttactttttt ctaagaagat ctgggtttata tttttctact
541 aaaggaacat caaagnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
601 atttatgtgt nnctggcagg caaaaaaaa catggagcac cgactannnn nnnnnnnnnn
661 nnnnnnccta acaaaagcggg agggcccccga gacctgaaaa tgctctgtgc agaagaagag
721 cagagtagga cgtgctgggt gaccgcgatt agattgctta agnnnnnnnn nnnnnnnnnn
781 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
841 nnnagaagta tatcagagaa ttccctggta gcaatggant tctcaggcca gaaaagcaga
901 gttatagaaa atccnnntga agccctttca gttgcnnntg aagaaggact cgcttgaggg
961 nnnnnnnnnn nnttacgnnt gggcactcac ggtagcccca ctgcctcttc acagagctct
1021 gccacaaaca tggctatcca ccggtcccaag ccatggtttc accacaaaat ttctagagat

1081 gaggtcagc gattgattat tcagcaagga cttgtggatg gnnnttttctt ggtacgggat
 1141 agtcagagta accccaaaac ttctgtactg tcaatgagtc atggacaaaa aataaagcac
 1201 tttcaaatta taccagtaga agatgacggt gaaatgttcc acacactgga tgatggccac
 1261 acaagattta cagatctaata acagctgggt gagttctatc aactcaataa gggcggttctt
 1321 ccttgcaagt tgaaacatta ttgtgctag ag

L6 ANSWER 75 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AY419442 GenBank (R)
 GenBank ACC. NO. (GBN): AY419442
 GenBank VERSION (VER): AY419442.1 GI:39775399
 CAS REGISTRY NO. (RN): 629064-34-2
 SEQUENCE LENGTH (SQL): 1362
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Genome Survey Sequence
 DATE (DATE): 17 Dec 2003
 DEFINITION (DEF): Homo sapiens ***GRB14*** gene, VIRTUAL TRANSCRIPT,
 partial sequence, genomic survey sequence.
 KEYWORDS (ST): GSS
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

COMMENT:

These sequences were made by sequencing genomic exons and ordering
 them based on alignment.

REFERENCE: 1 (bases 1 to 1362)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Inferring nonneutral evolution from human-chimp-mouse
 orthologous gene trios
 JOURNAL (SO): Science, 302 (5652), 1960-1963 (2003)
 REFERENCE: 2 (bases 1 to 1362)
 AUTHOR (AU): Clark,A.G.; Glanowski,S.; Nielson,R.; Thomas,P.;
 Kejariwal,A.; Todd,M.A.; Tanenbaum,D.M.; Civello,D.R.;
 Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
 White,T.J.; Sninsky,J.J.; Adams,M.D.; Cargill,M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (16-NOV-2003) Celera Genomics, 45 West Gude
 Drive, Rockville, MD 20850, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1362	/organism="Homo sapiens" /mol-type="genomic DNA" /db-xref="taxon:9606"
gene	<1..>1362	/gene="GRB14" /locus-tag="HCM6892"

SEQUENCE (SEQ):

1 atgagtttga gtgcaagaag agtcactctg cctgcaataa cgccaataat tctacagaaa
 61 agnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 121 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 181 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn aaagaacaat agaagaccac
 241 gaactggtga ttgaagtgtc atccaactgg gggatagaag aagaaaacaa actatacttt
 301 agaaaaaatt atgccaaata tgagttcttt aaaaacccaa tgnnnnnnnnnn nnnnnnnnnnnn
 361 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 421 ttcttgagtt caagcacata tcctgaaatt catggtttct tacatgcgaa agaacaggga
 481 aagaagtctt ggaaaaaaat ttactttttt ctaagaagat ctggtttata tttttctact
 541 aaaggaacat caaagnaacc gcggcatttg cagtttttca gcgaatttgg caatagtgtat
 601 atttatgtgt cactggcagg caaaaaaaa catggagcac cgactaacta tggattctgc
 661 tttaagccta acaaaagcggg agggccccga gacctgaaaa tgctctgtgc agaagaagag
 721 cagagtagga cgtgctgggt gaccgcgatt agattgctta agnnnnnnnnnn nnnnnnnnnnnn
 781 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 841 nnnagaagta tatcagagaa ttccctggta gcaatggact tctcaggcca gaaaagcaga
 901 gttatagaaa atcccactga agccctttca gttgcggttg aagaaggact cgcttggagg
 961 aaaaaaggat gtttacgcct gggcactcac ggtagcccca ctgcctcttc acagagctct
 1021 gccacaaaca tggctatcca ccggtcccg ccatggtttc accacaaaat ttctagagat
 1081 gaggtcagc gattgattat tcagcaagga cttgtggatg gagtttttctt ggtacgggat
 1141 agtcagagta accccaaaac ttctgtactg tcaatgagtc atggacaaaa aataaagcac
 1201 tttcaaatta taccagtaga agatgacggt gaaatgttcc acacactgga tgatggccac
 1261 acaagattta cagatctaata acagctgggt gagttctatc aactcaataa gggcggttctt

1321 ccttgcaagt tgaacatta ttgtgctagg attgctctct ag

L6 ANSWER 76 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC053559 GenBank (R)
GenBank ACC. NO. (GBN): BC053559
GenBank VERSION (VER): BC053559.1 GI:31657223
CAS REGISTRY NO. (RN): 535081-55-1
SEQUENCE LENGTH (SQL): 1872
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 12 Nov 2003
DEFINITION (DEF): Homo sapiens growth factor receptor-bound protein 14,
mRNA (cDNA clone MGC:61485 IMAGE:6162863), complete
cds.
KEYWORDS (ST): MGC
SOURCE: Homo sapiens (human)
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

COMMENT:

Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 115 Row: m Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4758477.

REFERENCE:

1 (bases 1 to 1872)
AUTHOR (AU): Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
Jordan, H.; Moore, T.; Max, S.I.; Wang, J.; Hsieh, F.;
Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
Gibbs, R.A.; Fahey, J.; Helton, E.; Kettelman, M.; Madan, A.;
Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;
Myers, R.M.; Butterfield, Y.S.; Krzywinski, M.I.;
Skalska, U.; Smailus, D.E.; Schnerch, A.; Schein, J.E.;
Jones, S.J.; Marra, M.A.

TITLE (TI): Generation and initial analysis of more than 15,000
full-length human and mouse cDNA sequences
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
(2002)

OTHER SOURCE (OS): CA 138:131969

REFERENCE:

2 (bases 1 to 1872)
AUTHOR (AU): Strausberg, R.
TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-JUN-2003) National Institutes of Health,
Mammalian Gene Collection (MGC), Cancer Genomics
Office, National Cancer Institute, 31 Center Drive,
Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1872	/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="MGC:61485 IMAGE:6162863" /tissue-type="skin, melanotic melanoma." /clone-lib="NIH-MGC-72" /lab-host="DH10B" /note="Vector: pCMV-SPORT6"
gene	1..1872	/gene="GRB14" /db-xref="LocusID:2888" /db-xref="MIM:601524"
CDS	12..1634	/codon-start=1 /product="growth factor receptor-bound protein 14" /protein-id="AAH53559.1" /db-xref="GI:31657224" /db-xref="LocusID:2888" /translation="MTTSLQDQGQSAASRAAARDS PLAAQVCGAAQGRGDAHDLAPAPW LHARALLPLPDGTRGCAADRRKKKDLDPPEMP PSPNPFPPELCCSPFTSVLSADLFPKA NSRKKQVIKVYSEDETSRALDVPSDITARDVCQL LILKNHYIDHDSWTLFEHLPHIGV ERTIEDHELVEVLSNWGIEEENKLYFRKNYAKY EFFKNPMYFFPEHMVSFATETNGE ISPTQILQMFLSSSTYPEIHGFLHAKEQGKKS WKKIYFFLRRSGLYFSTKGTSKEPRH LQFFSEFGNSDIYVSLAGKKKHGAPTNYGFCFKP NKAGGPRDLKMLCAEEEQSRTCWV TAIRLLKYGMQLYQNYMHPYQGRSGCSSQSISPM RSISENSLVAMDFSGQKSRVIENP TEALSAVEEGLAWRKKKGCLRLGTHGSPTASSQS SATNMAIHRSPWFHHKISRDEAQ RLIIQQGLVDGVFLVRDSQSNPKTFVLMSHGQK IKHFQIIPVEDDGEMFHTLDDGHT RFTDLIQLVEFYQLNKGVLPCCLKHYCARIAL" /note="RA; Region: Ras association (RalGDS/AF-6) domain" /db-xref="CDD:smart00314"
misc-feature	327..587	/note="PH; Region: Pleckstrin homology domain" /db-xref="CDD:smart00233"
misc-feature	714..1031	/note="SH2; Region: Src homology 2 domains" /db-xref="CDD:cd00173"

SEQUENCE (SEQ):

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121 acgacctggc gccggccccc tggctgcacg cgcgagcgct cctgcccctt ccggacggga
181 cccgcggctg tgctgcagac aggagaaaaa agaaagatct tgatgttccg gaaatgcat
241 ctattccaaa cccttttcct gagctatgct gttctccatt tacatctgtt ttgtcagcag
301 acctatttcc caaagcaaatt tcaaggaaaa aacagggtgat taaagtatac agtgaagatg
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1801 ctttacattc atcatttaa attcattagt taaaattaaa ccttaggaaa aaaatgaaaa
1861 aaaaaaaaaa aa

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L6 ANSWER 77 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AK074599 GenBank (R)
 GenBank ACC. NO. (GBN): AK074599
 GenBank VERSION (VER): AK074599.1 GI:22760142
 CAS REGISTRY NO. (RN): 453084-12-3
 SEQUENCE LENGTH (SQL): 1513
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 3 Sep 2002
 DEFINITION (DEF): Homo sapiens cDNA FLJ90118 fis, clone HEMBA1006916,
 highly similar to Homo sapiens ***Grb14*** mRNA.
 SOURCE: Homo sapiens embryo, 10 weeks whole embryo, mainly head
 cDNA to mRNA, clone_lib:HEMBA1 clone:HEMBA1006916.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 432 a 399 c 346 g 336 t

COMMENT:

NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo, Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
 sequencing and clone selection: Helix Research Institute (supported
 by Japan Key Technology Center etc.).

REFERENCE: 1
 AUTHOR (AU): Isogai,T.; Ota,T.; Nishikawa,T.; Hayashi,K.; Otsuki,T.;
 Sugiyama,T.; Suzuki,Y.; Nagai,K.; Sugano,S.; Ishii,S.;
 Kawai-Hio,Y.; Saito,K.; Yamamoto,J.; Wakamatsu,A.;
 Nakamura,Y.; Kojima,S.; Nagahari,K.; Masuho,Y.; Ono,T.;
 Okano,K.; Yoshikawa,Y.; Aotsuka,S.; Sasaki,N.;
 Hattori,A.; Okumura,K.; Iwayanagi,T.; Ninomiya,K.

TITLE (TI): NEDO human cDNA sequencing project

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 1513)

AUTHOR (AU): Isogai,T.; Otsuki,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (25-MAR-2002) Takao Isogai, Helix Research
 Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
 Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
 Tel:81-438-52-3975, Fax:81-438-52-3986)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1513	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="HEMBA1006916" /tissue-type="whole embryo, mainly head" /clone-lib="HEMBA1" /dev-stage="embryo, 10 weeks" /note="cloning vector: pME18SFL3"

SEQUENCE (SEQ):

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181  tagcccccac gccctttcac agagctctgc cacaaacatg gctatccacc ggtcccagcc
241  atggtttcac cacaaaattt cctccgcctc ccccccctcc ccgcccctc gcagatagct
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1441 tacaaataag caaagacttg gattgacttt acattcatca tttaaaattc attagttaaa
1501 attaaacctt agg

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L6 ANSWER 78 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BC021820 GenBank (R)
 GenBank ACC. NO. (GBN): BC021820
 GenBank VERSION (VER): BC021820.1 GI:18256069
 CAS REGISTRY NO. (RN): 387318-13-0
 SEQUENCE LENGTH (SQL): 870
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 16 Apr 2003
 DEFINITION (DEF): Mus musculus growth factor receptor bound protein 14,
 mRNA (cDNA clone IMAGE:3967891), partial cds.
 SOURCE:
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 277 a 183 c 209 g 201 t
 COMMENT:

Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H.; Garcia, A.M.; Lu, X.; Hulyk, S.W.; Loulseged, H.;
 Kowis, C.R.; Sneed, A.J.; Martin, R.G.; Muzny, D.M.; Nanavati,
 A.N.; Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 40 Row: g Column: 24.

REFERENCE: 1 (bases 1 to 870)
 AUTHOR (AU): Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
 Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
 Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
 Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
 Jordan, H.; Moore, T.; Max, S.I.; Wang, J.; Hsieh, F.;
 Diatchenko, L.; Marusina, K.; Farmer, A.A.; Rubin, G.M.;
 Hong, L.; Stapleton, M.; Soares, M.B.; Bonaldo, M.F.;
 Casavant, T.L.; Scheetz, T.E.; Brownstein, M.J.;
 Usdin, T.B.; Toshiyuki, S.; Carninci, P.; Prange, C.;
 Raha, S.S.; Loquellano, N.A.; Peters, G.J.; Abramson, R.D.;
 Mullahy, S.J.; Bosak, S.A.; McEwan, P.J.; McKernan, K.J.;
 Malek, J.A.; Gunaratne, P.H.; Richards, S.; Worley, K.C.;
 Hale, S.; Garcia, A.M.; Gay, L.J.; Hulyk, S.W.;
 Villalon, D.K.; Muzny, D.M.; Sodergren, E.J.; Lu, X.;
 Gibbs, R.A.; Fahey, J.; Helton, E.; Kettelman, M.; Madan, A.;
 Rodrigues, S.; Sanchez, A.; Whiting, M.; Madan, A.;
 Young, A.C.; Shevchenko, Y.; Bouffard, G.G.;
 Blakesley, R.W.; Touchman, J.W.; Green, E.D.;
 Dickson, M.C.; Rodriguez, A.C.; Grimwood, J.; Schmutz, J.;

Myers,R.M.; Butterfield,Y.S.; Krzywinski,M.I.;
Skalska,U.; Smailus,D.E.; Schnerch,A.; Schein,J.E.;
Jones,S.J.; Marra,M.A.

TITLE (TI): Generation and initial analysis of more than 15,000
full-length human and mouse cDNA sequences
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
(2002)

OTHER SOURCE (OS): CA 138:131969
REFERENCE: 2 (bases 1 to 870)

AUTHOR (AU): Strausberg,R.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (18-JAN-2002) National Institutes of Health,
Mammalian Gene Collection (MGC), Cancer Genomics
Office, National Cancer Institute, 31 Center Drive,
Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..870	/organism="Mus musculus" /mol-type="mRNA" /strain="FVB/N" /db-xref="taxon:10090" /clone="IMAGE:3967891" /tissue-type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone-lib="NCI-CGAP-Mam1" /lab-host="DH10B" /note="Vector: pCMV-SPORT6"
gene	<1..870	/gene="Grb14" /db-xref="LocusID:50915"
CDS	<1..625	/db-xref="MGI:1355324" /gene="Grb14" /codon-start=2 /product="Grb14 protein" /protein-id="AAH21820.1" /db-xref="GI:18256070" /db-xref="LocusID:50915" /db-xref="MGI:1355324" /translation="VTAIRLLKDGMLYQNYMHP YQGRSACNSQSMSPMRVSSENSLV AMDFSGEKSRVIDNPTEALSVAVEEGLAWRKKGC LRLGNHGSPSAPSQSSAVNMALHR SQPWFHHRISRDEAQRLLIRQGPVDGVFLVRDSQ SNPRTFVLMSHKGQKIKHYQIIPV EDDGELFHTLDDGHTKFTDLIQLVEFYQLNRGVL PCKLKHYCARMAV"

SEQUENCE (SEQ):

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L6 ANSWER 79 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF329696 GenBank (R)
GenBank ACC. NO. (GBN): AF329696
GenBank VERSION (VER): AF329696.1 GI:13161041
CAS REGISTRY NO. (RN): 325452-27-5
SEQUENCE LENGTH (SQL): 3815
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates

DATE (DATE): 14 May 2001
 DEFINITION (DEF): Homo sapiens tankyrase 2 mRNA, complete cds.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 1120 a 788 c 924 g 983 t
 REFERENCE: 1 (bases 1 to 3815)
 AUTHOR (AU): Lyons,R.J.; Deane,R.; Lynch,D.K.; Ye,Z.S.;
 Sanderson,G.M.; Eyre,H.J.; Sutherland,G.R.; Daly,R.J.
 TITLE (TI): Identification of a novel human tankyrase through its
 interaction with the adaptor protein ***Grb14***
 JOURNAL (SO): J. Biol. Chem., 276 (20), 17172-17180 (2001)
 OTHER SOURCE (OS): CA 135:118599
 REFERENCE: 2 (bases 1 to 3815)
 AUTHOR (AU): Lyons,R.J.; Deane,R.; Lynch,D.K.; Ye,Z.-S.J.;
 Sanderson,G.M.; Eyre,H.J.; Sutherland,G.R.; Daly,R.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (17-DEC-2000) Cancer Research, Garvan
 Institute of Medical Research, 384 Victoria St.,
 Sydney, NSW 2010, Australia

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..3815	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="10" /map="10q23.2"
CDS	140..3640	/codon-start=1 /product="tankyrase 2" /protein-id="AAK13463.1" /db-xref="GI:13161042" /translation="MSGRRRCAGGGAACASAAAEA VEPAARELFEACRNGDVERVKRLV TPEKVNSRDITAGRKSTPLHFAAGFGRKDVVEYLL QNGANVQARDDGGLIPLHNACSGF HAEVVNLLLRHGADPNARDNWNYPHEAAIKGK IDVCIVLLQHGAEPTIRNTDGRTA LDLADPSAKAVLTGEYKKDELLESARSGNEEKMM ALLTPLNVNCHASDGRKSTPLHLA AGYNRVKIVQLLLQHGADVHAKDKGDLVPLHNAC SYGHYEVELLVKHGACVNAMDLW QFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHN KSAIDLAPTPQLKERLAYEFKGHS LLQAAREADVTRIKKHLSELMVNFKHPQTHETAL HCAAASPYPKRKQICELLRLKGAN INEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV NALDNLGQTS LHRAAYCGHLQTCR LLLSYGCDPNIISLQGFTALQMGNENVQQLLQEG ISLGNSEADRQLLEAAKAGDVETV KKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVV EYLLQHGADVHAKDKGGLVPLHNA CSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAA AKGKYEICKLLQHGADPTKKNRD GNTPLDLVKDGDITDIQDLLRGDAALLDAAKKGCL ARVKKLSSPDNVNCRDTQGRHSTP LHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPL HNAASYGHVDVAALLIKYNACVNA TDKWAFTPLHEAAQKGRQQLCALLAHGADPTLK NQEGQTPLDLVSADDVSALLTAAM PPSALPSCYKPQVLNGVRSPGATADALSSGPSSP SSLSAASSLDNLSGSFSELSSVVS SSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHL MDIFEREQITLDVLVEMGHKELKE IGINAYGHRHKLKIGVERLISGQQLNPYLTLNT SGSGTILIDLS PDDKEFQSVEEEM QSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLW ERYTHRRKEVSEENHNHANERMLF HGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAEN SSKSNQYVYGIGGGTGCPVHKDRS CYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGH HSVTGRPSVNLALAEYVIYRGEQ AYPEYLITYQIMRPEGMVDG"

SEQUENCE (SEQ):

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3121 tctcaagatt cagaaggttt gtaacaagaa actatgggaa agatacactc accggagaaa
3181 agaagtttct gaagaaaacc acaaccatgc caatgaacga atgctatttc atgggtctcc
3241 ttttgtgaat gcaattatcc acaaaggctt tgatgaaagg catgcgtaca taggtggtat
3301 gtttggagct ggcatttatt ttgctgaaaa ctcttccaaa agcaatcaat atgtatatgg
3361 aattggagga ggtactgggt gtccagttca caaagacaga tcttgttaca tttgccacag
3421 gcagctgctc ttttgccggg taacctttgg aaagtctttc ctgcagttca gtgcaatgaa
3481 aatggcacat tctcctccag gtcatcactc agtcactggt aggccctg agaatggcct
3541 agcattagct gaatatgtta ttacagagg agaacaggct tatcctgagt atttaattac
3601 ttaccagatt atgaggcctg aaggatggt cgatggataa atagttattt taagaaacta
3661 attccactga acctaaaatc atcaaagcag cagtggcctc tacgttttac tctttgctg
3721 aaaaaaaatc atcttgccca caggcctgtg gcaaaaggat aaaaatgtga acgaagtta
3781 acattctgac ttgataaagc ttaataatgt tacag

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L6 ANSWER 80 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB560608 GenBank (R)
GenBank ACC. NO. (GBN): BB560608
GenBank VERSION (VER): BB560608.1 GI:9646974
CAS REGISTRY NO. (RN): 284994-84-9
SEQUENCE LENGTH (SQL): 323
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 1 Aug 2000

DEFINITION (DEF): BB560608 RIKEN full-length enriched, 10 days neonate olfactory brain Mus musculus cDNA clone E530113B02 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.

ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 92 a 89 c 53 g 89 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 323)

AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..323	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E530113B02" /clone-lib="RIKEN full-length enriched, 10 days neonate olfactory brain" /tissue-type="olfactory brain" /dev-stage="10 days neonate" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

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1 gctgttctcc actttttccc ccggtcgatt ttacccctc tactgggggt tccttcccc
61 ctacctgcta ccctcacttt ccccgatgg ctgttcaccc ccactttctt tcactcgtta
121 cactacagaa gaagaagcat ccaaaggagt atgataacag agagagagag agatcaccag
181 gctgaaaacc catcatggtg gaaaggagat ttcacctccg gggtaccaa acaaataggt
241 cacacattgc aaattagtga aaacttgat tcctattaca ctcatgactt taaatttatt
301 agttaaatt aaaccctttt aac

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L6 ANSWER 81 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB560607 GenBank (R)
 GenBank ACC. NO. (GBN): BB560607
 GenBank VERSION (VER): BB560607.1 GI:9646973
 CAS REGISTRY NO. (RN): 284994-83-8
 SEQUENCE LENGTH (SQL): 313
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB560607 RIKEN full-length enriched, 10 days neonate olfactory brain Mus musculus cDNA clone E530113B01 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 100 a 76 c 54 g 83 t
 COMMENT:

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 313)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;

Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..313	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E530113B01" /clone-lib="RIKEN full-length enriched, 10 days neonate olfactory brain" /tissue-type="olfactory brain" /dev-stage="10 days neonate" /lab-host="DH10B" /note="site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTT TTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 ccacctatat ccagttggtg gacttccacc agcttaacag gcggtccttc cttccacact
61 gaaccacact tctgttagga cgctgttca cccctcctct gtttactct ttacaccaca
121 gaagaagaag gattctaagg agaatgatca gagagagaga gagagatcac aaggctgcaa
181 acatatcatg ctgaaaagga gatttcacct gcgggttacc aaaaaaata ggtcacacat
241 tccaaattag tgcaaacctg gatttcattt acatcatga ctttaaattt attagttaaa
301 attaaacctt att
  
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L6 ANSWER 82 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB559554 GenBank (R)
 GenBank ACC. NO. (GBN): BB559554
 GenBank VERSION (VER): BB559554.1 GI:9645920
 CAS REGISTRY NO. (RN): 284984-30-1
 SEQUENCE LENGTH (SQL): 334
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB559554 RIKEN full-length enriched, 2 days pregnant
 adult female ovary Mus musculus cDNA clone E330039G15
 3' similar to AF076619 Rattus norvegicus molecular
 adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 117 a 90 c 41 g 86 t
 COMMENT:

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 Sciences Center(GSC), Yokohama Institute
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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
 ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
 ,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

REFERENCE: 1 (bases 1 to 334)
 AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
 Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
 Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
 Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
 Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamuta,T.;
 Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..334	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330039G15" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'

GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTT
TTTTTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. Second strand cDNA
was prepared with the primer
adapter of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAATTAATCC
CCCCCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. Vector: a
modified pBluescript KS(+) after
bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 gtacttcaca tacatcatcc acctctagac tttcaccaat ttccacaccc ctttccttcc
61 ctttccacct gaaccaccac tgtccactga ttccccctct ccccaacttt ctctcacttc
121 ctacactaca gaagaagaag gatccaaagg agaatcatta gagagagaga gagagatcac
181 aaggctgaaa accaatcatg gtgaaaagaa gatttcacct ccggcttaca aaaacaaata
241 ggtcacacat tccaaattag tgaaaacttg gattcctatt acactcatga ctttaaatatt
301 attagttaaa attaaacctt attaaaaaaa tagg

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L6 ANSWER 83 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB559080 GenBank (R)
GenBank ACC. NO. (GBN): BB559080
GenBank VERSION (VER): BB559080.1 GI:9645446
CAS REGISTRY NO. (RN): 284979-54-0
SEQUENCE LENGTH (SQL): 319
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 1 Aug 2000
DEFINITION (DEF): BB559080 RIKEN full-length enriched, 2 days pregnant
adult female ovary *Mus musculus* cDNA clone E330037E03
3' similar to AF076619 *Rattus norvegicus* molecular
adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE:
ORGANISM (ORGN): *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 108 a 62 c 62 g 87 t

COMMENT:

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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 319)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;

Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.,; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330037E03" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

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1 tgtttacaga cctgatccag ccgctggaat tcaacctcct taactggggg tccttccttc
61 catgctgaag cattattctg ctaggacggc tggtatcccc aactttgttt cactcgtcac
121 actacagtag aagaaggatg caaaggagaa tgattagaga gagagagaga gatcacaagg
181 ctgaaaacaa atcatggtga aaagaagatt tcacctgcgg gttacaaaaa aaaatagggtc
241 acacattgca aattagtga aacttggatt cctattacac tcatgacttt aaatttatta
301 gttaaaatta aaccttatt
  
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L6 ANSWER 84 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB558470 GenBank (R)
 GenBank ACC. NO. (GBN): BB558470
 GenBank VERSION (VER): BB558470.1 GI:9644836
 CAS REGISTRY NO. (RN): 284973-44-0
 SEQUENCE LENGTH (SQL): 250
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB558470 RIKEN full-length enriched, 2 days pregnant
 adult female ovary Mus musculus cDNA clone E330034C06
 3' similar to AF076619 Rattus norvegicus molecular
 adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE:
 ORGANISM (ORGN): Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 74 a 54 c 49 g 73 t

COMMENT:

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 250)

Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO):

unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..250	/organism="Mus musculus" /db-xref="taxon:10090" /clone="E330034C06" /clone-lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female" /tissue-type="ovary" /dev-stage="2 days pregnant adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTT TTTTTTTTTN 3'], cDNA was prepared

by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. Second strand cDNA
was prepared with the primer
adapter of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAATTAATCC
CCCCCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. Vector: a
modified pBluescript KS(+) after
bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 ctttagcagc tgaatgaat gctgacagat cccctacaca gatactgcag gtgttttttaa
61 gctccagcac gtatcctgaa atccatggct tcttacatgc aaaggaacag ggaaagaagt
121 cttggaaaaa agcttacttt tttctcagaa gatctggctt atattttttt actaaaggca
181 catccaagga accacggcat ttgcagcttt tcagtgaatt cagcactagt cacgtttata
241 tgtcactggc

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L6 ANSWER 85 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB519321 GenBank (R)
GenBank ACC. NO. (GBN): BB519321
GenBank VERSION (VER): BB519321.1 GI:9570779
CAS REGISTRY NO. (RN): 284222-57-7
SEQUENCE LENGTH (SQL): 319
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 28 Jul 2000
DEFINITION (DEF): BB519321 RIKEN full-length enriched, 16 days neonate
heart Mus musculus cDNA clone D830035H10 3' similar to
AF076619 Rattus norvegicus molecular adapter rGrb14 (
Grb14) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 106 a 71 c 58 g 84 t
COMMENT:

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 319)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;

Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	/organism="Mus musculus" /db-xref="taxon:10090" /clone="D830035H10" /clone-lib="RIKEN full-length enriched, 16 days neonate heart" /tissue-type="heart" /dev-stage="16 days neonate" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTT TTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 acttcacaga cctccttcca gctcgtggct tctaccagct caacaggggc tccttccctc
61 caagctgaac cattactttg ctaggatggc cgtttacccc aactttgtct cactcgttac
121 actacagaag aagaaggatc cataggagaa tgatcagaga gagagagaga gatcactagg
181 ctgaaaacaa atcatgggtga aaagaagatt tcacctgcgg gttacaaaaa ataataggtc
241 acacattgca aattagtga aacttggatt cctattacac tcatgacttt aaatttatta
301 gttaaaatta aaccttatt
  
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L6 ANSWER 86 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB360808 GenBank (R)
 GenBank ACC. NO. (GBN): BB360808
 GenBank VERSION (VER): BB360808.1 GI:9072636
 CAS REGISTRY NO. (RN): 279052-46-9
 SEQUENCE LENGTH (SQL): 231
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 12 Jul 2000
 DEFINITION (DEF): BB360808 RIKEN full-length enriched, adult male corpus
 striatum Mus musculus cDNA clone C030049M20 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.
 SOURCE:
 ORGANISM (ORGN): house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 87 a 45 c 38 g 61 t
 COMMENT:

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length

CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 231)

Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
 Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
 Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
 Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
 Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
 Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
 Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
 Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
 Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
 Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
 Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.;
 Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
 Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
 Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
 Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..231	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="C030049M20" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

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1 cctgttcagc ccaactctgt ctactccct acactacaga agaagaagga ttcacagggtg
61 tatgattaga gagagaaaga gagatcaca ggctgaaaac aaatcatggt gtaaagaaga
121 tttcacctgc ggcttaccaa aaaaaatagg tcacacattc caaattagtg aaaacttggg
181 ttcctattac actcatgact ttaaatttat tagttaaaat taaaccttat t
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L6 ANSWER 87 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB360354 GenBank (R)
GenBank ACC. NO. (GBN): BB360354
GenBank VERSION (VER): BB360354.1 GI:9072182
CAS REGISTRY NO. (RN): 279047-92-6
SEQUENCE LENGTH (SQL): 284
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 Jul 2000
DEFINITION (DEF): BB360354 RIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030046J22 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 103 a 53 c 54 g 74 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 284)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;

Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..284	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="C030046J22" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATAATATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

```

1 agctcaacag gggggtcctt cttccaagc tgaaccatca ctgtgctagg atggctgttt
61 agccaaactt tctttcactc ttacactac agaagaagaa ggatcccaag gagaatgatt
121 agagagagag agagagatca caaggctgaa aacaaatcat ggtgaaaaga agatttcacc
181 tccgggttac aaaaaaaaaat aggtcacaca ttgcaaatta gtgaaaactt ggattcctat
241 tacactcatg actttaaat tattagttaa aattaaacct tatt
  
```

L6 ANSWER 88 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB359872 GenBank (R)
 GenBank ACC. NO. (GBN): BB359872
 GenBank VERSION (VER): BB359872.1 GI:9071700
 CAS REGISTRY NO. (RN): 279043-10-6
 SEQUENCE LENGTH (SQL): 245
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 12 Jul 2000
 DEFINITION (DEF): BB359872 RIKEN full-length enriched, adult male corpus
 striatum Mus musculus cDNA clone C030043M21 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 92 a 55 c 40 g 58 t

COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 245)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T. y;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T. a;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..245	/organism="Mus musculus" /strain="C57BL/6j" /db-xref="taxon:10090" /clone="C030043M21" /clone-lib="RIKEN full-length enriched, adult male corpus striatum" /sex="male" /tissue-type="corpus striatum" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'
GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT
TTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
10.0 and subtraction to Rot =
185.0. second strand cDNA was
prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCC 3']. cDNA was cloned
into the XhoI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

```

1 accatccac gacgcccgt cccccctact gtgtttcact cgatacacca cagaagaaga
61 aggatcccaa ggagaatgat tagagagaga gagagagatc acaagcctga aaacaaatca
121 tgctgaaaag aagatttcac ctccgggtta caaaaaaaaa tagttcacac attccaaatt
181 agtggaaact tggattccta ttacactctt gactttaaat ttattagtta aaattaaacc
241 ttatt

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L6 ANSWER 89 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB319216 GenBank (R)
GenBank ACC. NO. (GBN): BB319216
GenBank VERSION (VER): BB319216.1 GI:9026251
CAS REGISTRY NO. (RN): 278502-24-2
SEQUENCE LENGTH (SQL): 311
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 11 Jul 2000
DEFINITION (DEF): BB319216 RIKEN full-length enriched, adult male corpora
quadrigemina Mus musculus cDNA clone B230379D24 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 89 a 69 c 61 g 92 t
COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 311)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;

Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
 Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
 Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..311	/organism="Mus musculus" /db-xref="taxon:10090" /clone="B230379D24" /clone-lib="RIKEN full-length enriched, adult male corpora quadrigemina" /sex="male" /tissue-type="corpora quadrigemina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 tatcccaaat tcgaattttt taagaacccc atgtatttct ttccagagca catggtgtct
61 tttagcagctg aaatgaatgg tgacagatcc cctacacagg tactgcaggt gttttaagc
121 tccagcacgt atcctgaaat ccacggcttc ttacatgcaa aggaacaggg aaagaagtct
181 tggaaaaaag cttacttttt tctcagaaga tctggctcat atttttctac taaaggcaca
241 tccaaggaac cacggcattt gcagcttttc agtgaattca gcactagtca cgtttatatg
301 tcactggcag g
  
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L6 ANSWER 90 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB283308 GenBank (R)
 GenBank ACC. NO. (GBN): BB283308
 GenBank VERSION (VER): BB283308.1 GI:8983757
 CAS REGISTRY NO. (RN): 278048-97-8
 SEQUENCE LENGTH (SQL): 503

MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Aug 2000
 DEFINITION (DEF): BB283308 RIKEN full-length enriched, adult retina Mus
 musculus cDNA clone A930101L21 3' similar to AF076619
 Rattus norvegicus molecular adapter rGrb14 (
 Grb14) mRNA, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 162 a 97 c 113 g 131 t

COMMENT:

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 The Institute of Physical and Chemical Research (RIKEN)
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 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
 ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
 ,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 503)
 Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
 Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
 Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
 Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
 Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
 Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..503	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A930101L21" /clone-lib="RIKEN full-length enriched, adult retina" /tissue-type="retina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental
Animal Research in Riken
contributed to prepare mouse
tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT
TTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
20.0 and subtraction to Rot =
459.0. Second strand cDNA was
prepared with the primer adapter
of sequence
[5'GAGAGAGAGATTCTCGAGTTAATTAAATTAA
TCCCCCCCCCCCCC 3']. cDNA was
cleaved with XhoI and BamHI.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. ~Retina RNA was
provided by Stefano Gustincich,
Department of Neurobiology,
Harvard Medical School, 220
Longwood Ave., Boston, MA02115,
USA, whose assistance we
gratefully acknowledge

SEQUENCE (SEQ):

```

1 aggctcggcc gctgatcatt ccgcggggcc tctggatgga gttttcttgt tacggatagt
61 tcagagtaac cccagaactt ttgtactgtc aatgagtcac ggacaaaaga taaaacacta
121 tcaaattata cccgtagaag atgatggtga gctgttccat actctggatg atggccatac
181 gaagttcaca cacctcatcc agctggtgga gttctaccag ctcaacaggg gggtccttcc
241 ttgcaagctg aagcattact gtgctaggat ggctgtttag ccaaactgtt tgtcactcgt
301 tacactacag aagaagaagg atgcaaagga gaatgattag agagagagag agagatcaca
361 aggctgaaaa caaatcatgg tgaaaagaag atttcacctg cgggttacaa aaaaaaatag
421 gtcacacatt ccaaattagt gaaaacttgg attcctatta cactcatgac tttaaattta
481 gttagttaaa attaaacctt att

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L6 ANSWER 91 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB282445 GenBank (R)
GenBank ACC. NO. (GBN): BB282445
GenBank VERSION (VER): BB282445.1 GI:8982894
CAS REGISTRY NO. (RN): 278040-34-9
SEQUENCE LENGTH (SQL): 281
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 1 Aug 2000
DEFINITION (DEF): BB282445 RIKEN full-length enriched, adult retina Mus
musculus cDNA clone A930037N11 3' similar to AF076619
Rattus norvegicus molecular adapter rGrb14 (
Grb14) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 92 a 86 c 37 g 66 t
COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 281)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..281	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A930037N11" /clone-lib="RIKEN full-length enriched, adult retina" /tissue-type="retina" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'GAGAGAGAGATTCTCGAGTTAATTAAATTAA TCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we

gratefully acknowledge

SEQUENCE (SEQ):

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1 ccgtatccct tccatcccca cctgatagta tccctcccca tcccacgcct cccctcgccc
61 tacatccccc tcaattcact acaccacaga gaagcaggat cccccccgac aatcactaga
121 gagagagaga gagattacaa ccctgaaaac aaatcatggt gacaagaaga ttttaccccc
181 gggttacaaa agaaaatagc tcacacattg caaattagtg aaaacttgga ttctattac
241 attcatgact ttaaatttat tagttaaaat taaaccttac t
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L6 ANSWER 92 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB191006 GenBank (R)
GenBank ACC. NO. (GBN): BB191006
GenBank VERSION (VER): BB191006.1 GI:8851625
CAS REGISTRY NO. (RN): 276734-11-3
SEQUENCE LENGTH (SQL): 276
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 30 Jun 2000
DEFINITION (DEF): BB191006 RIKEN full-length enriched, adult male spinal
cord Mus musculus cDNA clone A330065D15 3' similar to
AF076619 Rattus norvegicus molecular adapter rGrb14 (
Grb14) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 97 a 62 c 45 g 72 t

COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

1 (bases 1 to 276)
AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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source          1..276      /organism="Mus musculus"
                               /db-xref="taxon:10090"
                               /clone="A330065D15"
                               /clone-lib="RIKEN full-length
                               enriched, adult male spinal cord"
                               /sex="male"
                               /tissue-type="spinal cord"
                               /dev-stage="adult"
                               /lab-host="DH10B"
                               /note="Site-1: SalI; site-2:
                               BamHI; cDNA library was prepared
                               and sequenced in Mouse Genome
                               Encyclopedia Project of Genome
                               Exploration Research Group in
                               Riken Genomic Sciences Center and
                               Genome Science Laboratory in
                               RIKEN. Division of Experimental
                               Animal Research in Riken
                               contributed to prepare mouse
                               tissues. 1st strand cDNA was
                               primed with a primer [5'
                               GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT
                               TTTTTTTVN 3'], cDNA was prepared
                               by using trehalose
                               thermo-activated reverse
                               transcriptase and subsequently
                               enriched for full-length by
                               cap-trapper. cDNA went through one
                               round of normalization to Rot =
                               10.0 and subtraction to Rot =
                               459.0. Second strand cDNA was
                               prepared with the primer adapter
                               of sequence [5'
                               GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
                               CCCCCCCCCC 3']. cDNA was cleaved
                               with XhoI and BamHI. Vector: a
                               modified pBluescript KS(+) after
                               bulk excision from Lambda FLC I. "
=====

```

SEQUENCE (SEQ):

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1 cctgggatcc ttcccttcaa gctgcaacat cactttgcta ggacgcccgt taacccaac
61 tctgtttcac tcattacacc acagaaggag aaggatcaa aggagaatga ttagagagag
121 agagagagat cacaaggctg aaaacaattc atcgtgaaaa gcagatttca cctccggctt
181 accaaaataa atagttcaca cattccaaat tagtgaaaac ttggattcct attacactca
241 tgacttttaa tttattagtt aaaattaaac cttatt

```

L6 ANSWER 93 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB187252 GenBank (R)
 GenBank ACC. NO. (GBN): BB187252
 GenBank VERSION (VER): BB187252.1 GI:8847823
 CAS REGISTRY NO. (RN): 276657-85-3
 SEQUENCE LENGTH (SQL): 289
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 30 Jun 2000
 DEFINITION (DEF): BB187252 RIKEN full-length enriched, adult male spinal
 cord Mus musculus cDNA clone A330041E09 3' similar to
 AF076619 Rattus norvegicus molecular adapter rGrb14 (
 Grb14) mRNA, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 105 a 51 c 58 g 75 t

COMMENT:

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Email: genome-res@gsc.riken.go.jp,

URL:<http://genome.gsc.riken.go.jp/>
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE: 1 (bases 1 to 289)
 AUTHOR (AU): Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..289	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A330041E09" /clone-lib="RIKEN full-length enriched, adult male spinal cord" /sex="male" /tissue-type="spinal cord" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after

SEQUENCE (SEQ):

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1 ttaccagctc aaaagggggc tccttccttg caagctgaac cataactgtg ctaggatggc
61 tgttttagcct tactctgttt cactcgttac actacagaag aagaaggatg caaaggagaa
121 tgatcagaga gagagagaga gatcacaagg ctgaaaacaa atcatgggtga aaagaagatt
181 tcacctgagg gttacaaaaa aaaataggtc acacattgca aattagttaa aacttggatt
241 cctattacac tcatgacttt aaatttatta gttaaaatta aaccttatt

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L6 ANSWER 94 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB184777 GenBank (R)
 GenBank ACC. NO. (GBN): BB184777
 GenBank VERSION (VER): BB184777.1 GI:8845348
 CAS REGISTRY NO. (RN): 276633-09-1
 SEQUENCE LENGTH (SQL): 215
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 30 Jun 2000
 DEFINITION (DEF): BB184777 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330015N04 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 87 a 32 c 38 g 58 t

COMMENT:

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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

REFERENCE:

1 (bases 1 to 215)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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source      1..215      /organism="Mus musculus"
                        /db-xref="taxon:10090"
                        /clone="A330015N04"
                        /clone-lib="RIKEN full-length
                        enriched, adult male spinal cord"
                        /sex="male"
                        /tissue-type="spinal cord"
                        /dev-stage="adult"
                        /lab-host="DH10B"
                        /note="Site-1: SalI; site-2:
                        BamHI; cDNA library was prepared
                        and sequenced in Mouse Genome
                        Encyclopedia Project of Genome
                        Exploration Research Group in
                        Riken Genomic Sciences Center and
                        Genome Science Laboratory in
                        RIKEN. Division of Experimental
                        Animal Research in Riken
                        contributed to prepare mouse
                        tissues. 1st strand cDNA was
                        primed with a primer [5'
                        GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTT
                        TTTTTTTVN 3'], cDNA was prepared
                        by using trehalose
                        thermo-activated reverse
                        transcriptase and subsequently
                        enriched for full-length by
                        cap-trapper. cDNA went through one
                        round of normalization to Rot =
                        10.0 and subtraction to Rot =
                        459.0. Second strand cDNA was
                        prepared with the primer adapter
                        of sequence [5'
                        GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
                        CCCCCCCCCC 3']. cDNA was cleaved
                        with XhoI and BamHI. Vector: a
                        modified pBluescript KS(+) after
                        bulk excision from Lambda FLC I. "
=====

```

SEQUENCE (SEQ):

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1 ttgtttcatt ccttacacca cagaagaaga acgatccaaa ggagtatgat tagagagaga
61 gagagagatc acaaggctga aaacaaatca tggtgaaaag aagatttcac ctgcgggtta
121 caaaaaaaaa taggtcacac attgcaaatt agtgaaaact tggattccta ttacattcat
181 gacttttaaat ttattagtta aaattaaacc ttatt

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L6 ANSWER 95 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC):          BB173204      GenBank (R)
GenBank ACC. NO. (GBN): BB173204
GenBank VERSION (VER): BB173204.1 GI:8832287
CAS REGISTRY NO. (RN): 276506-98-0
SEQUENCE LENGTH (SQL): 282
MOLECULE TYPE (CI):   mRNA; linear
DIVISION CODE (CI):   Expressed sequence tag
DATE (DATE):          29 Jun 2000
DEFINITION (DEF):     BB173204 RIKEN full-length enriched, adult male
                        hypothalamus Mus musculus cDNA clone A230044K20 3'
                        similar to AF076619 Rattus norvegicus molecular adapter
                        rGrb14 ( ***Grb14*** ) mRNA, mRNA sequence.

SOURCE:               house mouse.
ORGANISM (ORGN):      Mus musculus
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                        Euteleostomi; Mammalia; Eutheria; Rodentia;
                        Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 98 a 55 c 55 g 74 t
COMMENT:

```

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Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 282)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..282	/organism="Mus musculus" /db-xref="taxon:10090" /clone="A230044K20" /clone-lib="RIKEN full-length enriched, adult male hypothalamus" /sex="male" /tissue-type="hypothalamus" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

SEQUENCE (SEQ):

1 gctcaacagg gggtccttcc ttcccagctg aagcattact gtgctaggat gctgttttac
 61 cctaactctg tgtcactcgt tacactacag tagaagaagg atgcaaagga gaatgatcag
 121 agagagagag agagatcaca agcctgaaaa caaatcatgg tgtaaagaag atttcacctg
 181 cgggttacca aaaaaaatag gtcacacatt ccaaattagt gaaaacttgg attcctatta
 241 cactcatgac tttaaattta ttagttaaaa ttaaacctta tt

L6 ANSWER 96 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB170892 GenBank (R)
 GenBank ACC. NO. (GBN): BB170892
 GenBank VERSION (VER): BB170892.1 GI:8829975
 CAS REGISTRY NO. (RN): 276483-86-4
 SEQUENCE LENGTH (SQL): 259
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 29 Jun 2000
 DEFINITION (DEF): BB170892 RIKEN full-length enriched, adult male
 hypothalamus Mus musculus cDNA clone A230022B15 3'
 similar to AF076619 Rattus norvegicus molecular adapter
 rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 79 a 55 c 45 g 80 t
 COMMENT:

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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE: 1 (bases 1 to 259)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
 Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
 Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
 Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
 Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
 Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
 Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
 Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
 Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
 Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
 Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.;
 Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
 Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
 Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
 Hayashizaki, Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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1..259

/organism="Mus musculus"
/db-xref="taxon:10090"
/clone="A230022B15"
/clone-lib="RIKEN full-length
enriched, adult male hypothalamus"
/sex="male"
/tissue-type="hypothalamus"
/dev-stage="adult"
/lab-host="DH10B"
/note="Site-1: SalI; site-2:
BamHI; cDNA library was prepared
and sequenced in Mouse Genome
Encyclopedia Project of Genome
Exploration Research Group in
Riken Genomic Sciences Center and
Genome Science Laboratory in
RIKEN. Division of Experimental
Animal Research in Riken
contributed to prepare mouse
tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
TTTTTTVN 3'], cDNA was prepared
by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
20.0 and subtraction to Rot =
459.0. Second strand cDNA was
prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCC 3']. cDNA was cleaved
with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after
bulk excision from Lambda FLC I. "

SEQUENCE (SEQ):

1 cctgatatta tacacctaaa atgcatgcag acagatccct tacacagata ctgcacgtgt
61 ttttaagctc cagcacctat cctgaaatcc atggcttctt tcatccaaag gaacagggaa
121 agaattattg gaaaaaagct tacttttttt tcagaagatt tggcttatat ttttttacta
181 aaggcacatc caaggaacca tggcatttgc agcttttcag tgaattcagc actagtcacg
241 tttatatgtc actggcagg

L6 ANSWER 97 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB124451 GenBank (R)
GenBank ACC. NO. (GBN): BB124451
GenBank VERSION (VER): BB124451.1 GI:8777019
CAS REGISTRY NO. (RN): 275947-71-2
SEQUENCE LENGTH (SQL): 312
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 27 Jun 2000
DEFINITION (DEF): BB124451 RIKEN full-length enriched, adult male urinary
bladder Mus musculus cDNA clone 9530097N18 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.

SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 108 a 60 c 60 g 84 t

COMMENT:

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 312)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.; Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.; Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.; Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yamanaka,I.; Yano,R.H.; Yasunishi,A.; Yokota,T.; Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..312	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530097N18" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATAATCC CCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after

SEQUENCE (SEQ):

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1 gacttcatcc agcttgtgga gttttaccac ctctacaggg gggtccttcc ttgcaacctg
61 aagcttcact ttgctaggaa ggcaatttac cccaactgtc tgcactcat tacactacag
121 aagaagaagg atcctaagga gaatgattag agagagagag agagatcaca aggctgaaaa
181 caaatcatgg tgaaaagaag atttcacctg cgggttacaa aaaaaaatag gtcacacatt
241 gctaattagt gaaaacttgg attcctatta cactcatgac tttaaattta ttagttaaaa
301 ttaaacctta tt

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L6 ANSWER 98 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB115268 GenBank (R)
 GenBank ACC. NO. (GBN): BB115268
 GenBank VERSION (VER): BB115268.1 GI:8767836
 CAS REGISTRY NO. (RN): 275855-88-4
 SEQUENCE LENGTH (SQL): 235
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 27 Jun 2000
 DEFINITION (DEF): BB115268 RIKEN full-length enriched, adult male urinary bladder Mus musculus cDNA clone 9530049M14 3' similar to AF076619 Rattus norvegicus molecular adapter rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 89 a 39 c 45 g 62 t
 COMMENT:

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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

1 (bases 1 to 235)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..235	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530049M14" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: Sali; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

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1 atggctgttt atccctactg cgtctcactc gttacactac agaaggagaa ggattctaag
61 gagaatgata agagagagag agagagatca caaggctgaa aacaaatcat ggtgaaaaga
121 agatttcacc tgcgggttac caaaaaaaaa taggtcacac attgcaaatt agtgaaaact
181 tggattccta ttacactcat gactttaaat ttattagtta aaattaaacc ttatt

```

L6 ANSWER 99 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB114126 GenBank (R)
GenBank ACC. NO. (GBN): BB114126
GenBank VERSION (VER): BB114126.1 GI:8766694
CAS REGISTRY NO. (RN): 275844-46-7
SEQUENCE LENGTH (SQL): 316
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 27 Jun 2000
DEFINITION (DEF): BB114126 RIKEN full-length enriched, adult male urinary
bladder Mus musculus cDNA clone 9530044F23 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 110 a 67 c 55 g 84 t

COMMENT:

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 316)
 Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..316	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530044F23" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cleaved

with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after
bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```
1 ccacagacct tatccagcac gtgcatttca ccagctccat aggggggtcc ttccttgcca
61 cctgaaacat tacttttctt ggaagcctct ttaccccaac ttgtttcac tccttacact
121 acagaagaag aaggatccaa aggagaatga tcagagagag agagagagat cactaggctg
181 aaaacaaatc atggtgaaaa gaagatttaa cctgcgggtt acaaaaaaaaa ataggtcaca
241 cattgcaaat tagtgaaaac ttggattcct attacactca tgactttaaa tttattagtt
301 aaaattaaac cttatt
```

L6 ANSWER 100 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB108361 GenBank (R)
GenBank ACC. NO. (GBN): BB108361
GenBank VERSION (VER): BB108361.1 GI:8760929
CAS REGISTRY NO. (RN): 275745-24-9
SEQUENCE LENGTH (SQL): 249
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 27 Jun 2000
DEFINITION (DEF): BB108361 RIKEN full-length enriched, adult male urinary
bladder Mus musculus cDNA clone 9530011B11 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 102 a 44 c 39 g 64 t
COMMENT:

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Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE: 1 (bases 1 to 249)
AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T. y;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T. a;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;
Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.;
Hayashizaki, Y.

TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al.)
JOURNAL (JO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..249	/organism="Mus musculus" /db-xref="taxon:10090" /clone="9530011B11" /clone-lib="RIKEN full-length enriched, adult male urinary bladder" /sex="male" /tissue-type="urinary bladder" /dev-stage="adult" /lab-host="DH10B" /note="site-1: Sali; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCC CCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

SEQUENCE (SEQ):

```

1 accctatatc tgcaaggatg actatttacc caaactatct ctactcatt acacaacaga
61 agaagaagga ttcaaaggag aatgattaga gagagagaga gatcacaagc ctgaaaacaa
121 atcatggtga aaagaagatt tcacctgcgg gttacaaaaa aaaataggtc acacattcca
181 aattagtga aacttggatt cctattacac tcatgacttt aaatttatta gttaaaatta
241 aaccttatt

```

L6 ANSWER 101 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB070600 GenBank (R)
GenBank ACC. NO. (GBN): BB070600
GenBank VERSION (VER): BB070600.1 GI:8580598
CAS REGISTRY NO. (RN): 273680-63-0
SEQUENCE LENGTH (SQL): 270
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 25 Jun 2000
DEFINITION (DEF): BB070600 RIKEN full-length enriched, 15 days embryo
male testis Mus musculus cDNA clone 8030491011 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.

SOURCE:
ORGANISM (ORGN):

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 93 a 57 c 45 g 75 t

COMMENT:

Contact: Yoshihide Hayashizaki
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URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

1 (bases 1 to 270)

AUTHOR (AU):

Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.; Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.; Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.; Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..270	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="8030491011" /clone-lib="RIKEN full-length enriched, 15 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="15 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 second strand cDNA was prepared with the primer adapter

of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAATTAATCC
CCCCCCCCCCCC 3']. cDNA was cloned
into the XhoI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

```

1 ctccttcctt ccttgctgca ccaatcctat gtttggatgc ctgcttaacc caactgtgtg
61 tcactcataa cactacagca gtagatggat ccaatggagg atgattagag agagagagag
121 agatcacaag cctgcaaaca aatcatgggtg aaaagaagat ttcacctccg gcttacaaaa
181 aaaaatagct cacacattgc aaattagtga aaacttggat tcctattaca ctcatgactt
241 taaatttatt agttaaaatt aaaccttatt

```

L6 ANSWER 102 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB045416 GenBank (R)
GenBank ACC. NO. (GBN): BB045416
GenBank VERSION (VER): BB045416.1 GI:8451802
CAS REGISTRY NO. (RN): 272392-50-4
SEQUENCE LENGTH (SQL): 323
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB045416 RIKEN full-length enriched, 13 days embryo
male testis *Mus musculus* cDNA clone 6030495A12 3'
similar to AF076619 *Rattus norvegicus* molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE:
ORGANISM (ORGN): house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; *Mus*
NUCLEIC ACID COUNT (NA): 113 a 63 c 59 g 88 t

COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 323)
Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
Kurihara, C.; Kusakabe, M.; Matsuyama, T.; Miki, R.;
Mizuno, Y.; Nakamura, M.; Oda, H.; Okazaki, Y.; Ono, T.;
Owa, C.; Saito, H.; Sakai, C.; Sato, K.; Shibata, K.;
Shibata, Y.; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.;
Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.;
Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.;
Yamanaka, I.; Yano, R. H.; Yasunishi, A.; Yokota, T.;

Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)

TITLE (TI):
JOURNAL (SO):

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..323	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030495A12" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

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1 attcccagtt ctcagacctt atccagctcc ggattacacc acttcacagg gggttccttc
61 cttccaaact gaagcattat tgtcctagga tggctgttta gccaaactct gtttcaatcg
121 ttacactaca gaagaagaag gatccaaagg agaatgatta gagagagaga gagagatcac
181 aaggctgtaa acaaatcatg gtgaaaagaa gatttcacct gcgggttaca aaaaaaata
241 ggtcacacat tgcaaattag tgaaaacttg gattcctatt acactcatga ctttaaattt
301 attagttaaa attaaacctt att
```

L6 ANSWER 103 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB042697 GenBank (R)
GenBank ACC. NO. (GBN): BB042697
GenBank VERSION (VER): BB042697.1 GI:8449083
CAS REGISTRY NO. (RN): 272365-31-8
SEQUENCE LENGTH (SQL): 289
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB042697 RIKEN full-length enriched, 13 days embryo
male testis Mus musculus cDNA clone 6030465G02 3'
similar to AF076619 Rattus norvegicus molecular adapter
rGrb14 (***Grb14***) mRNA, mRNA sequence.
SOURCE:
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 104 a 62 c 51 g 72 t

COMMENT:

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

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Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

REFERENCE:

1 (bases 1 to 289)

AUTHOR (AU):

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
Kurihara,C.; Kusakabe,M.; Matsuyama,T.; Miki,R.;
Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Ono,T.y;
Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
Shibata,Y.; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.;
Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I.; Yano,R.H; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL (SO):

Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..289	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030465G02" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared

by using trehalose
thermo-activated reverse
transcriptase and subsequently
enriched for full-length by
cap-trapper. cDNA went through one
round of normalization to Rot =
5.0 and subtraction to Rot =
100.0. Second strand cDNA was
prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC
CCCCCCCCCCC 3']. cDNA was cloned
into the XhoI and BamHI sites.
Vector: a modified pBluescript
KS(+) after bulk excision from
Lambda FLC I. Cloning sites, 5'
end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

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1 tctaccacta cacacggggt ctttcccccc aaccagcagc attactgtcc taggatcccc
61 gtttacccta actctgtgtc actcgttaca ccacagaaga agaaggatcc aaaggagaaat
121 gattagagag agagagagag atcacaaaggc tgaatacaaa tcatggtgaa aagaagattt
181 cacctgcggg ttacaaaaaa aaaatagggtc acacattgca aattagtgaa aacttggatt
241 cctattacac tcatgacttt aaatttatta gttaaaatta aaccttatt
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L6 ANSWER 104 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BB037605 GenBank (R)
GenBank ACC. NO. (GBN): BB037605
GenBank VERSION (VER): BB037605.1 GI:8443991
CAS REGISTRY NO. (RN): 272314-39-3
SEQUENCE LENGTH (SQL): 237
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 23 Jun 2000
DEFINITION (DEF): BB037605 RIKEN full-length enriched, 13 days embryo
forelimb Mus musculus cDNA clone 5930428012 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 84 a 50 c 40 g 63 t

COMMENT:

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
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N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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further details.

REFERENCE:

1 (bases 1 to 237)
AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
Hori, F.; Ishii, Y.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;

Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
 Kurihara,C.; Kusakabe,M.; Matsuyama,T. ; Miki,R.;
 Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y., Ono,T.y;
 Owa,C.; Saito,H.; Sakai,C.; Sato,K.; Shibata,K.;
 Shibata,Y.,; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
 Sogabe,Y.; Sugahara,Y., Suzuki,H.,; Suzuki,H.;
 Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
 Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
 Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
 Yoshida,K.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.;
 Hayashizaki,Y.

TITLE (TI): RIKEN Mouse ESTs (Konno,H., et al.)
 JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..237	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="5930428012" /clone-lib="RIKEN full-length enriched, 13 days embryo forelimb" /sex="mixed" /tissue-type="forelimb" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

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1 ggattgctct tttcccaaac tgtacctcac tccttacacc acaggagcag aaggatcccc
61 cggagaatga ttagagagag agagagaaat cacatggctg aaaacaaatc ttggtgaaaa
121 ccagatttca cctccgggtt accaaaaaaa ataggtcaca ctttccaaat tagtgaaaac
181 ttggattcct attacactca tgactttaaa tttattagtt aaaattaaac cttattg

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L6 ANSWER 105 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF155647 GenBank (R)
 GenBank ACC. NO. (GBN): AF155647
 GenBank VERSION (VER): AF155647.1 GI:7262856
 CAS REGISTRY NO. (RN): 259713-78-5
 SEQUENCE LENGTH (SQL): 1978
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 19 Mar 2000
 DEFINITION (DEF): Mus musculus adaptor protein ***GRB14*** (

Grb14) mRNA, complete cds.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 559 a 491 c 492 g 436 t

REFERENCE: 1 (bases 1 to 1978)
 AUTHOR (AU): Reilly,J.F.; Mickey,G.; Maher,P.A.
 TITLE (TI): Association of fibroblast growth factor receptor 1 with
 the adaptor protein ***Grb14*** . Characterization
 of a new receptor binding partner
 J. Biol. Chem., 275 (11), 7771-7778 (2000)
 OTHER SOURCE (OS): CA 132:330035

REFERENCE: 2 (bases 1 to 1978)
 AUTHOR (AU): Reilly,J.F.; Mickey,G.; Maher,P.A.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-JUN-1999) Cell Biology, The Scripps
 Research Institute, 10550 N. Torrey Pines Rd., CAL-3,
 La Jolla, CA 92037, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1978	/organism="Mus musculus" /db-xref="taxon:10090" /cell-line="NIH/3T3"
5' UTR	1..122	/gene="Grb14"
gene	1..1978	/gene="Grb14"
CDS	123..1739	/gene="Grb14" /note="member of Grb7 family" /codon-start=1 /product="adaptor protein GRB14" /protein-id="AAF43996.1" /db-xref="GI:7262857" /translation="MTTSLQDGGQSAAGRAGAQDS PLAVQVCRVAQGKGDAQDPAQVPG LHALSPASDATLRGAIDRRKMKDLDVLEKPPIPN PFPELCCSPLTSVLSAGLFPRANS RKKQVIKVYSEDETSRALEVPSDITARDVCQLLI LKNHYVDDNSWTLFEHLSHIGLER TVDEHLPTEVLSHWGEEDNKLYLRKNYAKYEF FKNPMYFFPEHMYVFAAEMNGDRS PTQILQVFLSSSTYPEIHGFLHAKEQGKKSWKKA YFFLRSGLYFSTKGTSKEPRHLQ LFSEFSTSHVYMSLAGKKKHGAPTPYGFCLKPNK AGGPRDLKMLCAEEEEQSRTCWVTA IRLLKDGMLYQNYMHPYQGRSACNSQSMSPMRS VSENSLVAMDFSGEKSRVIDNPTE ALSVAVEEGLAWRKKGCLRLGNHGSPSAPSQSSA VNMAHRSQPWFHHRISRDEAQRRL IIRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIK HYQIIPVEDDGELFHTLDDGHTKF TDLIQLVEFYQLNRGVLPCCLKHYCARMAY" /gene="Grb14"
3' UTR	1740..1978	

SEQUENCE (SEQ):

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1 gcggccctgc caccgcacct gcaaggcgct cgctgcctgc aaccgctcgg ctctgctcgc
61 ccccgaccct tcgtagcttt cgccctgcgg tcgatgactc cctagacccc tggcctacga
121 ccatgaccac gtccctgcaa gacgggcaga gcgccgcggg ccgggcaggc gcccaggatt
181 cgccgctggc agtgcagggtg tgccgcgttg cccagggcaa gggagacgcc caggaccctg
241 cgcagggtccc cggactgcac gcgctgtccc ccgcctccga tgcgaccctc cgcggtgcca
301 tagacaggag aaaaatgaaa gatctggatg ttctggaaaa gccacccatt cccaacccct
361 ttcctgagct ctgctgctct ccgcttacat ctgtgctgtc agcaggcctg tttcccaggg
421 ccaattcaag gaagaagcag gtgattaaag ttacagcga ggatgaaacc agcagagcat
481 tagagggtgcc cagtgcacatc acagcccagag atgtttgcca gctgttgatc ctgaagaacc
541 actatgtgga cgacaacagc tggacccttt ttgagcacct atctcacata ggtttagaaa
601 gaaccgtaga ggaccacgag ctgccaactg aagtgtctgtc tctactggga gtggaagaag
661 acaataagct gtatcttaga aagaattatg ccaaatatga attttttaag aaccctaatgt
721 atttctttcc agagcacatg gtgtcttttg cagctgaaat gaatggtgac agatccccta
781 cacagatact gcagggtgtt ttaagctcca gcacgtatcc tgaaatccat ggcttcttac
841 atgcaaagga acagggaaaag aagtctttgga aaaaagctta cttttttctc agaagatctg
901 gcttataattt ttctactaaa ggcacatcca aggaaccacg gcattttgcag cttttcagtg
961 aattcagcac tagtcacgtt tatatgtcac tggcaggaaa aaaaaaacac ggagcgccaa
1021 ctccctatgg attctgttta aagcctaaca aagcaggagg gccccgggac ctgaaaatgc
1081 tctgtgcaga agaagagcag agcaggacgt gctgggtgac cgccatccga ctgctgaagg

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1141 atggcatgca gctgtatcag aattatatgc atccatacca aggtagaagc gcctgcaatt
1201 ctccagagcat gtcacccatg agaagcgtat cagagaattc cctagtagca atggacttct
1261 cagggtgagaa gagcagagtc atagacaacc ccactgaagc gctttcgggt gctgttgagg
1321 aaggcctcgc gtggaggaaa aaaggctgtt tacgcctggg gaatcacgga agccccagtg
1381 cccctcccca gagctctgct gtgaacatgg ctctccatcg gtcccaacca tggtttcacc
1441 acagaatttc cagagatgag gctcagcggc tgatcattcg gcaggggcct gtggatggag
1501 ttttcttggt acgggatagt cagagtaacc ccagaacttt tgtactgtca atgagtcag
1561 gacaaaagat aaaacactat caaattatcc cgtagaaga tgatggtag ctgttcata
1621 ctctggatga tggccatacg aagttcacag acctatcca gctggtagg tttaccagc
1681 tcaacagggg ggtccttcct tgcaagctga agcattactg tgctaggatg gctgttttagc
1741 caaactgtgt gtcactcgtt acactacaga agaagaagga tgcaaaggag aatgattaga
1801 gagagagaga gagatcaca ggctgaaaac aaatcatggt gaaaagaaga ttccacctgc
1861 gggttacaaa aaaaaatagg tcacacattg caaattagtg aaaacttga ttcctattac
1921 actcatgact ttaaatattat tagttaaatt taaaccttat taaaaaaaa aaaaaaaa

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L6 ANSWER 106 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV362938 GenBank (R)
 GenBank ACC. NO. (GBN): AV362938
 GenBank VERSION (VER): AV362938.1 GI:6410585
 CAS REGISTRY NO. (RN): 249018-61-9
 SEQUENCE LENGTH (SQL): 207
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 14 Nov 1999
 DEFINITION (DEF): AV362938 RIKEN full-length enriched, 15 days embryo
 male testis Mus musculus cDNA clone 8030405L12 3'
 similar to AF076619 Rattus norvegicus molecular adapter
 rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 76 a 37 c 34 g 60 t
 COMMENT:

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE: 1 (bases 1 to 207)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.;
 Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
 Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.;
 Kai, C. ?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.;
 Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.;
 Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.;
 Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.;
 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.;
 Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.;
 Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.;
 Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.;
 Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al. 1999)
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..207	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="8030405L12" /clone-lib="RIKEN full-length enriched, 15 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="15 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCC CCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

```

1 attttttctc tacagcagga gaaggatccc aaggagaatg attagagaga gagagagaca
61 tcaccagcct gaaaacaaat tatgctgcac aggagatttc acctccggct tactaaagaa
121 aatagttcac acattccaaa ttagtgaaaa ctggattccc tattacaatc ttgactttaa
181 atttattagt taaaatttaa ccttatt

```

L6 ANSWER 107 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV355587 GenBank (R)
GenBank ACC. NO. (GBN): AV355587
GenBank VERSION (VER): AV355587.1 GI:6396644
CAS REGISTRY NO. (RN): 248828-30-0
SEQUENCE LENGTH (SQL): 231
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 12 Nov 1999
DEFINITION (DEF): AV355587 RIKEN full-length enriched, adult male adrenal
gland Mus musculus cDNA clone 7330413L18 3' similar to
AF076619 Rattus norvegicus molecular adapter rGrb14 (
Grb14) mRNA, mRNA sequence.

SOURCE:

ORGANISM (ORGN):

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 93 a 32 c 36 g 70 t

COMMENT:

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute

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 Email: genome-res@gsc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
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Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
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Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)

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 further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 231)

Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.;
 Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
 Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.;
 Kai, C. ?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.;
 Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.;
 Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.;
 Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.;
 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.;
 Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.;
 Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.;
 Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.;
 Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno, H., et al. 1999)

JOURNAL (SO):

Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..231	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="7330413L18" /clone-lib="RIKEN full-length enriched, adult male adrenal gland" /sex="male" /tissue-type="adrenal gland" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGAGAGAGATTCTCGAGTTAATTAATTAATCC
 CCCCCCCCCC 3']. cDNA was cloned
 into the XhoI and BamHI sites.
 Vector: a modified pBluescript
 KS(+) after bulk excision from
 Lambda FLC I. Cloning sites, 5'
 end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

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1 gctttttacc ctaattatct ttcaattttt atactacaga agaagaagca tccaaaggag
61 aatgattaga gagagagaga gaaatcaciaa ggctgaaaac aaattatggt gaaaagaaga
121 tttcacctgc gggttacaaa aaaaaatagt tcacacattg caaattagtg aaaacttgga
181 ttcctattac attcatgact ttaaatttat tagtttaaat taaaccttat t
  
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L6 ANSWER 108 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV335961 GenBank (R)
 GenBank ACC. NO. (GBN): AV335961
 GenBank VERSION (VER): AV335961.1 GI:6376013
 CAS REGISTRY NO. (RN): 248628-93-5
 SEQUENCE LENGTH (SQL): 193
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Nov 1999
 DEFINITION (DEF): AV335961 RIKEN full-length enriched, adult male medulla
 oblongata Mus musculus cDNA clone 6330578M15 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 73 a 32 c 35 g 52 t 1 others

COMMENT:

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE:

1 (bases 1 to 193)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.;
 Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
 Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.;
 Kai, C. ?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.;
 Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.;
 Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.;
 Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.;
 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.;
 Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.;
 Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.;
 Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.;
 Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al. 1999)
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..193	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6330578M15" /clone-lib="RIKEN full-length enriched, adult male medulla oblongata" /sex="male" /tissue-type="medulla oblongata" /dev-stage="adult" /lab-host="DH10B" /note="site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

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1 aagaaagaag ggatcccaag gagcatgatt agagagagag aagagataac caggctgcac
61 accaatcatg gtgcaaagaa gaattttcac ttctgggtaa ccnactaata gctcacacat
121 ttcaaattag tggaaacttg gattcctatt acattcatga ctttaaattt attagttaaa
181 attaaacctt att

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L6 ANSWER 109 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV327707 GenBank (R)
 GenBank ACC. NO. (GBN): AV327707
 GenBank VERSION (VER): AV327707.1 GI:6367759
 CAS REGISTRY NO. (RN): 248487-17-4
 SEQUENCE LENGTH (SQL): 286
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Nov 1999
 DEFINITION (DEF): AV327707 RIKEN full-length enriched, adult male medulla
 oblongata Mus musculus cDNA clone 6330436D10 3' similar
 to AF076619 Rattus norvegicus molecular adapter rGrb14
 (***Grb14***) mRNA, mRNA sequence.

SOURCE:
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 105 a 52 c 53 g 76 t

COMMENT:

Contact: Yoshihide Hayashizaki
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 Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.

Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE:

1 (bases 1 to 286)
 AUTHOR (AU): Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.;
 Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
 Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.;
 Kai, C.?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.;
 Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.;
 Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.;
 Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.;
 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.;
 Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.;
 Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.;
 Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.;
 Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al. 1999)
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..286	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6330436D10" /clone-lib="RIKEN full-length enriched, adult male medulla oblongata" /sex="male" /tissue-type="medulla oblongata" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAGAGAGAGATTCTCGAGTTAATTAATTAATCC
 CCCCCCCCCC 3']. cDNA was cloned
 into the XhoI and BamHI sites.
 Vector: a modified pBluescript
 KS(+) after bulk excision from
 Lambda FLC I. Cloning sites, 5'
 end: SalI; 3' end: BamHI"

SEQUENCE (SEQ):

```

1 gcaccagtca tcagggcctc cttcctccca aactgaagca ttattatgct aggatggctg
61 ttcagccata ctcttctcat tcttatacta cagaagaaga aggatgccaa aggagaatga
121 ttagagagag agagagagat cacaaggctg aaaacaaatc atggtgaaaa gaagatttca
181 cctgcgggtt acaaaaaaaaa ataggtcaca cattgcaaat tagtgaaaac ttggattcct
241 attacattca tgactttaaa tttattagtt aaaattaaac cttatt
  
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L6 ANSWER 110 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV321727 GenBank (R)
 GenBank ACC. NO. (GBN): AV321727
 GenBank VERSION (VER): AV321727.1 GI:6291562
 CAS REGISTRY NO. (RN): 247815-00-5
 SEQUENCE LENGTH (SQL): 253
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 9 Nov 1999
 DEFINITION (DEF): AV321727 RIKEN full-length enriched, 13 days embryo
 male testis Mus musculus cDNA clone 6030436014 3'
 similar to AF076619 Rattus norvegicus molecular adapter
 rGrb14 (***Grb14***) mRNA, mRNA sequence.
 SOURCE:
 ORGANISM (ORGN): house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 84 a 46 c 45 g 78 t
 COMMENT:

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

REFERENCE:

AUTHOR (AU): 1 (bases 1 to 253)
 Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
 Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.;
 Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
 Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.;
 Kai, C. ?; Kawai, J.; Kikuchi, N.; Kojima, Y.; Koya, S.;
 Kusakabe, M.; Matsuyama, T.; Miki, R.; Mizuno, Y.;
 Nakamura, M.; Oda, H.; Okazaki, Y.; Owa, C.; Ozawa, Y.;
 Saito, H.; Sano, M.; Sato, K.; Shibata, K.; Shibata, Y.;
 Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.;
 Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.;
 Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.;
 Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.;
 Yoshino, M.; Muramatsu, M.; Hayashizaki, Y.
 TITLE (TI): RIKEN Mouse ESTs (Konno, H., et al. 1999)
 JOURNAL (SO): unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..253	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="6030436014" /clone-lib="RIKEN full-length enriched, 13 days embryo male testis" /sex="male" /tissue-type="testis" /dev-stage="13 days embryo" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

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1 gcagccttac tgtgatcggc ttcctctttc cccaaactct cttttactcc tttatctaca
61 gtagaagcag gttgcaagcg agaatgatta gagagtgaga gtgagattac caggctgata
121 acaattcatg gtgaaaagaa gatttcacct gcgggttaca aaaaaaaata ggtcacacat
181 tgcaaattag tgaaaacttg gatttcctatt acattcatga ctttaaattt attagttaaa
241 attaaacctt att

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L6 ANSWER 111 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AV259119 GenBank (R)
GenBank ACC. NO. (GBN): AV259119
GenBank VERSION (VER): AV259119.1 GI:6246578
CAS REGISTRY NO. (RN): 246989-25-3
SEQUENCE LENGTH (SQL): 230
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 4 Nov 1999
DEFINITION (DEF): AV259119 RIKEN full-length enriched, adult male testis
(DH10B) Mus musculus cDNA clone 4930403H14 3' similar
to AF076619 Rattus norvegicus molecular adapter rGrb14
(***Grb14***) mRNA, mRNA sequence.
SOURCE: house mouse.
ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 103 a 27 c 34 g 66 t
COMMENT:
Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

REFERENCE:

AUTHOR (AU):

1 (bases 1 to 230)

Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.?.; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.; Kusakabe,M.; Matsuyama,T.; Miki,R.; Mizuno,Y.; Nakamura,M.; Oda,H.; Okazaki,Y.; Owa,C.; Ozawa,Y.; Saito,H.; Sano,M.; Sato,K.; Shibata,K.; Shibata,Y.; Shigemoto,Y.; Shiraki,T.; Sogabe,Y.; Sugahara,Y.; Suzuki,H.; Suzuki,H.; Takahashi,F.; Tateno,M.; Tominaga,N.; Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.; Yasunishi,A.; Yokota,T.; Yoshiki,A.; Yoshino,M.; Muramatsu,M.; Hayashizaki,Y.

TITLE (TI):

RIKEN Mouse ESTs (Konno,H., et al. 1999)

JOURNAL (SO):

Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..230	/organism="Mus musculus" /strain="C57BL/6J" /db-xref="taxon:10090" /clone="4930403H14" /clone-lib="RIKEN full-length enriched, adult male testis (DH10B)" /sex="male" /tissue-type="testis" /dev-stage="adult" /lab-host="DH10B" /note="Site-1: SalI; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCC

CCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

SEQUENCE (SEQ):

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1 atgttcttat ctaaacttct taatttaata cactaaagaa gaagaatgaa acaaagaaga
61 aagatcagag agagagagaa atattacaag gttgaaaaca aatcttggtg aaaagaagat
121 ttaacctgcg gggtacaaaa aaaaatagtt cacacattgc aaattagtga aaacttggat
181 tcctattaca atcatgactt taaatttatt agttaaattt aaaccttatt

```

L6 ANSWER 112 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF190121 GenBank (R)
GenBank ACC. NO. (GBN): AF190121
GenBank VERSION (VER): AF190121.1 GI:6018121
CAS REGISTRY NO. (RN): 244113-77-7
SEQUENCE LENGTH (SQL): 2052
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Rodents
DATE (DATE): 22 Nov 2000
DEFINITION (DEF): Rattus norvegicus growth factor receptor binding protein GRB7 (Grb7) mRNA, complete cds.
SOURCE: Norway rat.
ORGANISM (ORGN): Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NUCLEIC ACID COUNT (NA): 440 a 602 c 548 g 462 t
REFERENCE: 1 (bases 1 to 2052)
AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.; Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.; Burnol,A.F.
TITLE (TI): Identification of the rat adapter ****Grb14**** as an inhibitor of insulin actions
JOURNAL (SO): J. Biol. Chem., 273 (40), 26026-26035 (1998)
OTHER SOURCE (OS): CA 130:20710
REFERENCE: 2 (bases 1 to 2052)
AUTHOR (AU): Kasus-Jacobi,A.; Bereziat,V.; Perdereau,D.; Girard,J.; Burnol,A.F.
TITLE (TI): Evidence for an interaction between the insulin receptor and Grb7. A role for two of its binding domains, PIR and SH2
JOURNAL (SO): Oncogene, 19 (16), 2052-2059 (2000)
OTHER SOURCE (OS): CA 133:69252
REFERENCE: 3 (bases 1 to 2052)
AUTHOR (AU): Burnol,A.F.; Perdereau,D.; Kasus-Jacobi,A.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (27-SEP-1999) UPR 1524, CNRS, 9 rue Jules Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2052	/organism="Rattus norvegicus" /db-xref="taxon:10116" /tissue-type="liver"
gene	1..2052	/gene="Grb7"
CDS	50..1657	/gene="Grb7" /note="molecular adapter" /codon-start=1 /product="growth factor receptor binding protein GRB7" /protein-id="AAF01776.1" /db-xref="GI:6018122" /translation="MELDLSPSHLSSSPEDVCPT PGTPPETPPPPDNPPPGDVKRSQP LPIPSSRKLREEEFQATSLPSIPNPFPELCSPPS QKPILGGSSGARGLLPRDSSRLCV VKVYSEDGACRSVEVAAGATARHVCCEMLVQRAHA LSDENWGLVECHPYLALERGLDHD ESVVEVQEAWPVGGDSRFIFRKNFAKYELFKSP HTLFPEKMOVSSCLDTPGTGISHEDL IQNFLNAGSFPEIQGFLQLRGSGRGSGRKLWKRF

FCFLRRSGLYYSTKGTSKDPRHLQ
 YVADINESNVYVVTQGRKLYGIPTDFGFCVKPNK
 LRNGHKGLHIFCSEDEQSRTCWLS
 AFRLFKYGVQLYKNYQQAQSRHLRLSYLGSPLR
 SVSDNTLVAMDFSGHAGRVIENPQ
 EALSAATEEAQAWRKKTNHRLSLPTPCSGLSLSA
 AIHRTQPFHGRISREESQRLIGQ
 QGLVDGVFLVRESQRNPQGFVLSLCHLQKVKHYL
 ILPSEDEGCLYFSMDDGQTRFTDL
 LQLVEFHQLNRGILPCLLRHCCARVAL"

SEQUENCE (SEQ):

```

1  ctttgggtcc  cgggtgtcccg  ctcttcttgc  tggagttcct  ccagggtgcca  tggaaactgga
61 tctgagcccg  tctcatctca  gcagctcccc  agaagatgtg  tgcccaactc  ctgggacccc
121 tcccagagact  cctccgcccc  cggataaccc  tccgcccggc  gatgtgaagc  ggtctcagcc
181 tttgcccac  ccaagtagca  ggaaacttcg  agaagaggag  tttcaggcaa  cctctctacc
241 ctccatcccc  aaccccttcc  ccgagctctg  cagcccacct  tcacagaaac  ccattcttgg
301 tggttcctcc  ggtgctaggg  ggttgcttcc  tcgagactcc  agccgcctct  gtgtggtgaa
361 ggtgtacagt  gaagatggag  cctgccggtc  tgtggaagtg  gcggcaggcg  cgacggctcg
421 ccatgtgtgt  gagatgctgg  tgcagcgagc  tcacgccctg  agcgatgaga  actggggcct
481 ggtggagtgc  caccctatt  tggctctgga  gcggggtttg  gaggaccatg  agtctgtggt
541 agaagtgcag  gaggcctggc  ctgtgggtgg  agacagccgc  ttcattcttc  gtaaaaaactt
601 cgccaagtat  gaactcttca  agagccctcc  gcacaccctg  tcccagaaa  agatggtttc
661 cagctgtctg  gatacaccaa  caggcataatc  ccatgaagac  ctcatccaga  acttcttgaa
721 tgctggcagc  ttccctgaga  tccagggtct  cctgcagctt  cggggatcag  gccgggggtc
781 aggtcgaaag  ctttggaac  gattcttctg  ctctctgct  cggcttgcc  tctattactc
841 gaccaagggc  accttaagg  acctacagta  cctacagtac  gtggcagata  taaatgagtc
901 caatgtgtat  gtggtgaccc  agggccgcaa  gctgtatggg  ataccaccg  acttcggctt
961 ttgtgtcaag  cccaacaagc  ttcgaaatgg  ccacaagggg  ctccacatct  tctgcagcga
1021 ggatgagcag  agtcggactt  gctggctgtc  cgcttccgg  ctcttcaagt  acgggggtaca
1081 gctatataag  aattatcagc  agggccagtc  tcgtcacctg  cgcttatcgt  atttggggctc
1141 tccacccttg  aggagtgtct  cagataatac  cctggtggcc  atggacttct  ctggccatgc
1201 tgggcgtgtc  attgagaacc  cccaggaagc  tctgagtgt  gccacagagg  aagcccaggc
1261 ctggaggaag  aagacaaacc  accgtctcag  cctgccacc  ccgtgctccg  gcctgagcct
1321 cagtgcagct  atccatcgca  cccagccctg  gtttcatgga  cgaatctccc  gggaggagag
1381 ccagcggcta  attggacagc  agggcctggt  ggatggtgta  ttcctggtcc  gggagagcca
1441 gcggaacca  cagggttctg  ttctgtctct  gtgccatctg  cagaaagtca  aacattatct
1501 catcttgcca  agcgaagatg  aaggctgcct  ttacttcagc  atggatgacg  gccagacccg
1561 ttccacagac  ctgctgcagc  tggtggaatt  ccaccagctg  aaccgaggca  tcctgccctg
1621 cttgctgctg  cactgtgtgt  cccgtgtggc  cctctgaggc  cacacaagct  gttacagcca
1681 tggggctgct  tatcgccctt  ctgctccgtt  cagtggactc  ggtgcagatg  ggtgggagta
1741 taaacagatg  aagagctccc  cccacttttc  tcccactttt  tttttttacc  tccctcaggt
1801 aatgaaacat  cccccagccc  tgttcatccc  tgactcctgt  ccccaaagga  ggcattgtgg
1861 tcctctcccc  ttggtagagc  tcctgaggca  gtgaagggca  ttatgagagg  agtaggggca
1921 gcccggtggt  tctcatgccc  caccacact  ctgtacagac  tgagaggcca  gttgatctgc
1981 tctgttttat  accagtgata  ataaagatta  ttttttgata  caaaaaaaaa  aaaaaaaaaa
2041 aaaaaaaaaa  aa

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L6 ANSWER 113 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI928176 GenBank (R)
 GenBank ACC. NO. (GBN): AI928176
 GenBank VERSION (VER): AI928176.1 GI:5664140
 CAS REGISTRY NO. (RN): 241373-88-6
 SEQUENCE LENGTH (SQL): 319
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 8 Mar 2000
 DEFINITION (DEF): wo95a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2463064 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 90 a 54 c 48 g 127 t
 COMMENT:
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 399 Std Error: 0.00

Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 319)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index

JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..319	<p>/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2463064" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "</p>

SEQUENCE (SEQ):

```
1  ttcctaagg ttaatttta ctaatgaatt ttaaagtatg aatgtaaagt caatccaagt
61  ctttgcttat ttgcaatgca caaactatct tttgttaact tgcaggtgaa atacattctt
121 ttcacatgat aatgttttcg cccttatcta tggctcttta ttatttttct tgagtccttt
181 tccttcaata gttaataaag tcacttctgg cttgtctaga gagcaatcct agcacaataa
241 tgtttcaact tgcaagggaag aacgccctta ttgagttgat agaactccac cagctgtatt
301 agatctgtaa atcttgtgt
```

L6 ANSWER 114 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI870172 GenBank (R)

GenBank ACC. NO. (GBN): AI870172

GenBank VERSION (VER): AI870172.1 GI:5544140

CAS REGISTRY NO. (RN): 390159-63-4

SEQUENCE LENGTH (SQL): 745

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 7 Mar 2000

DEFINITION (DEF): w115e05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone

IMAGE:2424992 3' similar to TR:Q14449 Q14449

GRB14 . ;, mRNA sequence.

SOURCE: human.

ORGANISM (ORGN): Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 189 a 157 c 145 g 249 t 5 others

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1767 Std Error: 0.00

Seq primer: -40UP from Gibco
 High quality sequence stop: 414.
 REFERENCE: 1 (bases 1 to 745)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..745	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2424992" /clone-lib="NCI-CGAP-Ut1" /tissue-type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab-host="DH10B" /note="Organ: uterus; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

SEQUENCE (SEQ):

```

1 tcctaagggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcagggtgaaa tacattcitt
121 tcacatggta atgttttcgc ccttatttat ggtcttttat tatttttctt gagtcctttt
181 ccttcaatag tttaaataag tcaccttctg ggcttgtcta gagagcaatc cttagcacaat
241 aatgtttcaa cttgcaagga agaacgcctt tattgagttg atagaactcc accagctgta
301 ttagatctgt aaatcttctg tggccatcat ccagtgtgtg gaacatttca ccgtcatctt
361 ctactgggat aatttgaaag tgctttattt tttgtccatg actcattgac agtacgaaag
421 ttttgggggtt actctgacta tcccgtacca agaaaactcc atccacaagt ccttgctgaa
481 taatcaatcg ctgagcctca tctctagaaa tnttgtgggtg aaaccatggc tgggaccggt
541 ggatagccat gtntgtggca gagctctgtg aagagcagtg gggctaccgt gagtgcccag
601 gcgtaaacat ccttttttnc tccaagcgag tccctcttca accgcaactg aaaggggctt
661 ccgtgggatn ttctaatact ctgcttttcc tgccctgaga agtcattgct accagggaaa
721 tctctgtnta cctcctcata ggtga
  
```

L6 ANSWER 115 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI767914 GenBank (R)
 GenBank ACC. NO. (GBN): AI767914
 GenBank VERSION (VER): AI767914.1 GI:5234435
 CAS REGISTRY NO. (RN): 236629-01-9
 SEQUENCE LENGTH (SQL): 429
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 21 Dec 1999
 DEFINITION (DEF): wi99c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
 IMAGE:2401458 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 112 a 74 c 74 g 168 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 925 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 260.

REFERENCE: 1 (bases 1 to 429)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..429	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2401458" /clone-lib="NCI-CGAP-Kid12" /tissue-type="2 pooled tumors (clear cell type)" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```
1 ttttcctaag gtttaatttt aactaatgaa ttttaaata tgaatgtaa gtcaatccaa
61 gtctttgctt atttgcaatg cacaaactat ttttttgtaa cttgcagggtg aaatacattc
121 ttttcacatg ataatgtttt cgcccttatt tatggtcttt tattatittt cttgagtcct
181 tttccttcaa tagtttaata agtcacttct ggctgttcta gagagcaatc ctagcacaat
241 aatgtttcaa cttgcaagga agaacgccct tattgagttg atagaactcc accagctgtt
301 ttagatctgt aattttgggg tggccatatt cagggtgtgt gaacatttca ccgtcatctt
361 ctactggtat aattggaaaa gtgctttatt ntittgtcca tgactcttgg accgtaccaa
421 agttttggg
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L6 ANSWER 116 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI760945 GenBank (R)
GenBank ACC. NO. (GBN): AI760945
GenBank VERSION (VER): AI760945.1 GI:5176612
CAS REGISTRY NO. (RN): 236076-02-1
SEQUENCE LENGTH (SQL): 312
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 21 Dec 1999
DEFINITION (DEF): wi70e05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
IMAGE:2398688 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 90 a 54 c 46 g 122 t
COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 403 Std Error: 0.00
Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 312)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..312	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2398688" /clone-lib="NCI-CGAP-Kid12" /tissue-type="2 pooled tumors (clear cell type)" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```
1 tttcctaagg tttaatttta actaatgaat tttaaatgat gaatgtaaag tcaatccaag
61 tctttgctta ttgcaatgc acaaactatt tttttgtaac ttgcagggtga aatacattct
121 tttcacatga taacgttttc gcccttattt atgggtctttt attatttttc ttgagtcctt
181 ttccttcaat agtttaataa gtcacttctg gcttgtctag agagcaatcc tagcacaata
241 atgtttcaac ttgcaaggaa gaacgccctt attgagttga tagaactcca ccagctgtat
301 tagatctgta aa
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L6 ANSWER 117 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI695260 GenBank (R)
GenBank ACC. NO. (GBN): AI695260
GenBank VERSION (VER): AI695260.1 GI:4983160
CAS REGISTRY NO. (RN): 233989-40-7
SEQUENCE LENGTH (SQL): 408
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 16 Dec 1999
DEFINITION (DEF): wa02b08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
IMAGE:2296887 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 112 a 82 c 62 g 152 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 848 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 396.

REFERENCE: 1 (bases 1 to 408)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..408	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2296887" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```

1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
61 ttgcttatt tgcaatgcac aaactatttt tttgtaactt gcagggtgaaa tacattcttt
121 tcacatgata atgttttcgc ccttatttat ggtcttttat ttttttctt gagtcctttt
181 ccttcaatag ttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccg tcattctcta
361 cccatccaca agtccttgct gaataatcaa tcgctgagcc tcattctta
  
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L6 ANSWER 118 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI671320 GenBank (R)
 GenBank ACC. NO. (GBN): AI671320
 GenBank VERSION (VER): AI671320.1 GI:4851051
 CAS REGISTRY NO. (RN): 232699-27-3
 SEQUENCE LENGTH (SQL): 497
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 17 Dec 1999
 DEFINITION (DEF): wc29a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2316554 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 144 a 100 c 87 g 164 t 2 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 795 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 372.

REFERENCE: 1 (bases 1 to 497)

AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..497	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2316554" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```
1 gcctgccagt gacacataaa taccactatt gccaaattcg ctaaaaactg caaatgccgc
61 gggttcctttg atgttccttt agtagaaaaa tataaaccag atcttcttag aaaaaagtaa
121 atttttttcc aagacttctt tccctgttct ttcgcatgta agaaaccatg aatttcagga
181 tatgtgcttg aactcagaaa catctgcaaa atctgtgtgg gggatatttc accattgggt
241 tcagttgcaa aagataccat atgctctgga aaaaaataca ttgggttttt aaagaactca
301 tatttggcat aattttttct aaagtatagt ttgttttctt cttctatccc ccagttggat
361 agcacttcaa tcaccagttc gtggtcttct attgttcttt ctacacctat gtgaggcagg
421 tgctcanaaaa ggggtccagct gtggtcatca atgtaatgat tcttcaggat caacagctga
481 ncaacatctc gagccgt
```

L6 ANSWER 119 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI624682 GenBank (R)

GenBank ACC. NO. (GBN): AI624682

GenBank VERSION (VER): AI624682.1 GI:4649613

CAS REGISTRY NO. (RN): 230649-94-2

SEQUENCE LENGTH (SQL): 533

MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 14 Dec 1999

DEFINITION (DEF): ts43e12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone
IMAGE:2231374 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.

ORGANISM (ORGN): Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 144 a 104 c 91 g 193 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1696 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 401

POLYA=No.

REFERENCE: 1 (bases 1 to 533)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..533	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2231374" /clone-lib="NCI-CGAP-Ut1" /tissue-type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab-host="DH10B" /note="Organ: uterus; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

SEQUENCE (SEQ):

```
1 tcctaagggt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcagggtgaaa tacattcttt
121 tcacatggta atgttttcgc cttattttat ggtcttttat ttttttctt ggtcctttt
181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccg tcattctcta
361 ctgggtataat ttgaaagtc tttatttttt gtccatgact cattgacagt acgaaagttt
421 tggggttact ctgactatcc cgtaccaaga aaactccatc cacaagtcct tgctgaataa
481 tcaatcgctg agcctcatct ctagaatnt tgtgtgaacc atggctggga ccg
```

L6 ANSWER 120 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI610228 GenBank (R)
GenBank ACC. NO. (GBN): AI610228
GenBank VERSION (VER): AI610228.1 GI:4619395
CAS REGISTRY NO. (RN): 390132-63-5
SEQUENCE LENGTH (SQL): 701
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 13 May 1999
DEFINITION (DEF): tp15g09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone
IMAGE:2187904 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 179 a 144 c 132 g 242 t 4 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 803 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 406
POLYA=No.

REFERENCE: 1 (bases 1 to 701)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..701	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2187904" /clone-lib="NCI-CGAP-Gas4" /tissue-type="poorly differentiated adenocarcinoma with signet ring cell features" /lab-host="DH10B" /note="Organ: stomach; Vector: pCMV-SPORT6; site-1: SalI; Site-2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

SEQUENCE (SEQ):

```

1 ttctaagggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcagggtgaaa tacattcctt
121 tcacatggta atgttttcgc ccttatttat ggtcttttat tatttttctt gagtcccttt
181 ccttcaatag ttttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccg tcattcttcta
361 ctgggtataat ttgaaagtgc tctatttttt gtccatgact cattgacagt acgaaagttt
421 tgggggttact ctgactatcc cgtacaaaaa aactccatcc acaagtcctt gctgaataat
481 caatcgctga gcctcatctc tagaaatttt gtgggtgaaac catggctggg accggtggat
541 agccatgttt gtggcagagc tctgtgaaga gcagtggngc taccgtgagt gccagccgt
601 aaacatcctt ttttcttcc agcgagtcct tcttcaaccg caactgaaag ggcttcagnn
661 ggattttcta taactctgct tttctggcct gagaagtcca t

```

L6 ANSWER 121 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI609572 GenBank (R)
 GenBank ACC. NO. (GBN): AI609572
 GenBank VERSION (VER): AI609572.1 GI:4618739
 CAS REGISTRY NO. (RN): 230319-99-0
 SEQUENCE LENGTH (SQL): 368
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 14 May 1999
 DEFINITION (DEF): tw28a08.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone
 IMAGE:2260982 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 100 a 59 c 57 g 151 t 1 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 318 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 324
 POLYA=No.

REFERENCE: 1 (bases 1 to 368)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..368	/organism="Homo sapiens" /db-xref="taxon:9606"

/clone="IMAGE:2260982"
 /clone-lib="NCI-CGAP-Ov35"
 /tissue-type="tumor, 5 pooled (see description)"
 /lab-host="DH10B"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site-1: SalI; Site-2: NotI; This library represents the normalized version of NCI-CGAP-Ov23. Cloned unidirectionally. Primer: oligo dT. Average insert size 0.86 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies."

SEQUENCE (SEQ):

```

1 tttttttttt tttttttttt ttttttatgc atacacttct tggatttatt aatgctatag
61 ttctatgaaa tccatgagta aatatagaaa cattgaaatt ctttctctct ctttagagtt
121 ttcttggtac gggatagtc gagtaacccc aaaactttcg tactgtcaat gagtcacgga
181 caaaaaataa agcactttca aattatacca gtaagtaatt cgtgatttca catttggtga
241 ttagaaatga ccttaatgct aagcttttga tcttaatgca taagcttttg gaaacttttg
301 ttttcttttg gnccttttat taaatataat ttggcagctt gtgctttgac tagagccccc
361 cgtccgcc

```

L6 ANSWER 122 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI522272 GenBank (R)
 GenBank ACC. NO. (GBN): AI522272
 GenBank VERSION (VER): AI522272.1 GI:4436407
 CAS REGISTRY NO. (RN): 228602-27-5
 SEQUENCE LENGTH (SQL): 604
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 13 Apr 1999
 DEFINITION (DEF): ti84g01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2138736 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 160 a 118 c 118 g 208 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1380 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 308.

REFERENCE: 1 (bases 1 to 604)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..604	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:2138736" /clone-lib="NCI-CGAP-Kid11" /lab-host="DH10B" /note="Organ: kidney; Vector:

pt7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```

1  ttcttaaggt ttaattttta ctaatgaatt ttaaatagat aatgtaaagt caatccaagt
61  ctttgcttat ttgcaatgca caaactattt ttttgtaact tgcaggtgaa atacattctt
121  ttcatatgat aatgttttcg cccttattta tggcttttta ttatttttct tgagtccttt
181  tccttcaata gtttaataag tcacttctgg ctgtctaga gagcaatcct agcacaataa
241  tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
301  agatctgtaa atcttgtgtg gccatcatcc agtgtgtgga acatttcacc gtcattctct
361  actggtataa tttgaaagtg ctttattttt tgtccatgac tcattgacag tacgaaagtt
421  ttgggggttac tctgactatc ccgtaccaag aaaactccat ccacaagtcc ttgctgaata
481  atcaatcgct gagcctcatc tctagaaatt ttgtggtgaa accatggctg ggacccgtgg
541  atagccatgt ttgtggcaaa gcttctggaa gaggcagggg ggctccggga gtgccagggc
601  gtaa

```

L6 ANSWER 123 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI505286 GenBank (R)
 GenBank ACC. NO. (GBN): AI505286
 GenBank VERSION (VER): AI505286.1 GI:4403137
 CAS REGISTRY NO. (RN): 228210-72-8
 SEQUENCE LENGTH (SQL): 578
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 11 Mar 1999
 DEFINITION (DEF): vp98h08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092831 3' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
 SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 NUCLEIC ACID COUNT (NA): 148 a 135 c 111 g 179 t 5 others
 COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:599063
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 High quality sequence stop: 379.

REFERENCE: 1 (bases 1 to 578)
 AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.; Allen,M.; Bowers,Y.; Person,B.; Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.; Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.; Waterston,R.; Wilson,R.
 TITLE (TI): The WashU-NCI Mouse EST Project 1999
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
=====+	=====	=====

source 1..578

```

/organism="Mus musculus"
/db-xref="taxon:10090"
/clone="IMAGE:1092831"
/clone-lib="Stratagene mouse
diaphragm (#937303)"
/tissue-type="diaphragm"
/dev-stage="adult"
/lab-host="SOLR (kanamycin
resistant)"
/note="Organ: diaphragm; Vector:
pBluescript SK-; Site-1: EcoRI;
Site-2: XhoI; Cloned
unidirectionally from mRNA
prepared from diaphragm muscle.
Primer: oligo dT. Average insert
size: 1.5 kb. Uni-ZAP XR Vector;
~5' adaptor sequence: 5'
GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT

```

SEQUENCE (SEQ):

```

1 aataaggttt aattttaact aataaattta aaggcatgag tgtaatagga atccaagttt
61 tcactaattt gcaatgtgtg acctattttt ttttgaacc cgcaggtgaa atcttctttt
121 caccatggtt tgttttcagc cttgtgatct ctctctctct ctctaatacat tctcctttgc
181 atccttcttc ttctgtagtg taacgagtga cacacagttt ggctaaacag ccacacctagc
241 acagtaatgc ttcagcttgc aaggaaggac cccctgttg agctggtaga actccaccag
301 ctggatgagg tctgtgaact tcgtatggcc atcatccaga gtatggaaca gctcaccatc
361 atcttctacg ggtataatnt gatagtgttt tatcttttgt ccatgactca ttgacagtac
421 aaaagttctg gggttactct gactatcccg taccaagaaa actncatcca caggcccttg
481 ccgaatgatc agncgctgag cctcatctct tgaaatnctg tgggtgaaacc catgttggac
541 cgatggaaac catgttcaca ccanaactct ggaagggc

```

L6 ANSWER 124 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI494168 GenBank (R)
 GenBank ACC. NO. (GBN): AI494168
 GenBank VERSION (VER): AI494168.1 GI:4395171
 CAS REGISTRY NO. (RN): 228132-01-2
 SEQUENCE LENGTH (SQL): 368
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 13 Apr 1999
 DEFINITION (DEF): ti14f01.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2130457 5' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.

SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 98 a 71 c 58 g 141 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 416 Std Error: 0.00
 Seq primer: -40RP from Gibco.

REFERENCE: 1 (bases 1 to 368)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..368	/organism="Homo sapiens" /db-xref="taxon:9606"

/clone="IMAGE:2130457"
 /clone-lib="NCI-CGAP-Kid11"
 /lab-host="DH10B"
 /note="Organ: kidney; Vector:
 pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site-1: Not
 I; Site-2: Eco RI; Plasmid DNA
 from the normalized library
 NCI-CGAP-Kid3 was prepared, and ss
 circles were made in vitro.
 Following HAP purification, this
 DNA was used as tracer in a
 subtractive hybridization
 reaction. The driver was
 PCR-amplified cDNAs from a pool of
 5,000 clones made from the same
 library (cloneIDs 1322376-1323911,
 1456007-1456775, and
 1500552-1502855). subtraction by
 Bento Soares and M. Fatima
 Bonaldo. "

SEQUENCE (SEQ):

```

1 tcctaagggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
61 ttgtgttatt tgcaatgcac aaactatatt ttgtgaactt gcaggtgaaa tacattcttt
121 tcacatgata atgttttcgc cttattttat ggtcttttat tatttttctt gagtcctttt
181 ctttcaatag ttttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccg tcattcttctc
361 ctctgtgcc

```

L6 ANSWER 125 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI425417 GenBank (R)
 GenBank ACC. NO. (GBN): AI425417
 GenBank VERSION (VER): AI425417.1 GI:4271348
 CAS REGISTRY NO. (RN): 226504-01-4
 SEQUENCE LENGTH (SQL): 503
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 15 Mar 2000
 DEFINITION (DEF): my18a09.y1 Barstead mouse heart MPLRB3 Mus musculus
 cDNA clone IMAGE:696184 5' similar to TR:Q14449 Q14449
 GRB14 . ; , mRNA sequence.

SOURCE: house mouse.
 ORGANISM (ORGN): Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 103 a 171 c 143 g 86 t

COMMENT:

Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 MGI:429744
 Seq primer: -40RP from Gibco
 High quality sequence stop: 493
 POLYA=No.

REFERENCE: 1 (bases 1 to 503)
 AUTHOR (AU): Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;
 Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;
 Allen,M.; Bowers,Y.; Person,B. ; Swaller,T.;
 Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E. ;
 Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
 Waterston,R.; Wilson,R.
 TITLE (TI): The WashU-NCI Mouse EST Project 1999
 JOURNAL (SO): Unpublished (1999)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..503	/organism="Mus musculus" /strain="BALB/c" /db-xref="taxon:10090" /clone="IMAGE:696184" /clone-lib="Barstead mouse heart MPLRB3" /sex="mixed" /tissue-type="heart" /dev-stage="6 weeks" /lab-host="DH10B" /note="Organ: heart; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: EcoRI; Site-2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTT TTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [CTTGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

SEQUENCE (SEQ):

```

1 aattcggatc caaggcaagg cgctcgctgc ctgcaaccgc tcggctctgc tcgccccag
61 cccttcgtag ctttcgcctc gcggtcgatg actccctaga cccctggcct acgaccatga
121 ccacgtccct gcaagacggg cagagcgccg cgggccgggc aggcgcccag gattcgccgc
181 tggcagtgca ggtgtgccgc gttgcccg gcaagggaga cgccaggac ccggcgagg
241 tccccggact gcacgcgctg tccccgcct ccgatgacgac cctccgcggt gccatagaca
301 ggagaaaaat gaaagatctg gatgttctgg aaaagccacc cattccaac ccctttcctg
361 agctctgctg ctctccgctt acatctgtgc tgtcagcagg cctgtttccc agggccaatt
421 caaggaagaa gcaggtgatt aaagtttaca gcgaggatga aaccagcaga gcattagagg
481 tgcccagtga catcacagcc cga

```

L6 ANSWER 126 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI383743 GenBank (R)
GenBank ACC. NO. (GBN): AI383743
GenBank VERSION (VER): AI383743.1 GI:4196524
CAS REGISTRY NO. (RN): 225333-52-8
SEQUENCE LENGTH (SQL): 423
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 18 Mar 1999
DEFINITION (DEF): tc47e05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens
cDNA clone IMAGE:2067776 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 116 a 74 c 69 g 162 t 2 others

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 967 Std Error: 0.00
Seq primer: -40UP from Gibco.

REFERENCE: 1 (bases 1 to 423)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..423	/organism="Homo sapiens"

/db-xref="taxon:9606"
 /clone="IMAGE:2067776"
 /clone-lib="Soares-total-fetus-Nb2
 HF8-9w"
 /dev-stage="8-9 weeks"
 /lab-host="DH10B"
 /note="Vector: pT7T3D-Pac
 (Pharmacia) with a modified
 polylinker; Site-1: Not I; Site-2:
 Eco RI; 1st strand cDNA was
 prepared from mRNA obtained from
 pooled 8-9 week (total) fetus
 material with a Not I - oligo(dT)
 primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAAT
 TTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned
 into the Not I and Eco RI sites of
 the modified pT7T3 vector. Library
 went through one round of
 normalization, and was constructed
 by Bento Soares and M. Fatima
 Bonaldo. "

SEQUENCE (SEQ):

```

1 cctaagggtt aattttaact aatgaatttt aaatgatgaa tgtaaagtca atccaagtct
61 ttgcttattt gcaatgcaca aactattttt ttgtaacttg cagggtgaaat acattctttt
121 cacatgataa cgttttcgcc cttatttatg gtcttttatt atttttcttg agtccttttc
181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg
241 tttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag
301 atctgtaaat cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
361 tgggtataatt ngaaagtgct ttattntttt gtcatgactc attgacagta caaaagtttt
421 ggg
  
```

L6 ANSWER 127 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AI364971 GenBank (R)
 GenBank ACC. NO. (GBN): AI364971
 GenBank VERSION (VER): AI364971.1 GI:4124660
 CAS REGISTRY NO. (RN): 224494-55-7
 SEQUENCE LENGTH (SQL): 318
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 16 Feb 1999
 DEFINITION (DEF): qz41h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
 IMAGE:2029493 3' similar to TR:Q14449 Q14449
 GRB14 . ;, mRNA sequence.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 90 a 54 c 48 g 125 t 1 others
 COMMENT:
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 447 Std Error: 0.00
 Seq primer: -40UP from Gibco.
 REFERENCE: 1 (bases 1 to 318)
 AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
 Project (CGAP), Tumor Gene Index
 JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
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```

=====+=====+=====
source      1..318      /organism="Homo sapiens"
                        /db-xref="taxon:9606"
                        /clone="IMAGE:2029493"
                        /clone-lib="NCI-CGAP-Kid11"
                        /lab-host="DH10B"
                        /note="Organ: kidney; Vector:
                        pT7T3D-Pac (Pharmacia) with a
                        modified polylinker; Site-1: Not
                        I; Site-2: Eco RI; Plasmid DNA
                        from the normalized library
                        NCI-CGAP-Kid3 was prepared, and ss
                        circles were made in vitro.
                        Following HAP purification, this
                        DNA was used as tracer in a
                        subtractive hybridization
                        reaction. The driver was
                        PCR-amplified cDNAs from a pool of
                        5,000 clones made from the same
                        library (cloneIDs 1322376-1323911,
                        1456007-1456775, and
                        1500552-1502855). Subtraction by
                        Bento Soares and M. Fatima
                        Bonaldo. "
```

SEQUENCE (SEQ):

```

1 ttcctaaggt ttaattttta ctaatgaatt ttaaataatg aatgtaaagt caatccaagt
61 ctttgcttat ttgcaatgca caaactatct ttttgtaact tgcagggtgaa atacattctt
121 ttcacatgat aatgttttcg cccttatcta tggnccttta ttatttttct tgagtccttt
181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcct agcacaataa
241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
301 agatctgtaa atcttctg
```

L6 ANSWER 128 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

```

LOCUS (LOC):      AI263214      GenBank (R)
GenBank ACC. NO. (GBN): AI263214
GenBank VERSION (VER): AI263214.1 GI:3871417
CAS REGISTRY NO. (RN): 221598-25-0
SEQUENCE LENGTH (SQL): 382
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE):      3 Feb 1999
DEFINITION (DEF): qz36f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                  IMAGE:2028991 3' similar to TR:Q14449 Q14449
                  ***GRB14*** . ;, mRNA sequence.
```

```

SOURCE:          human.
ORGANISM (ORGN): Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                  Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                  Hominidae; Homo
```

NUCLEIC ACID COUNT (NA): 112 a 59 c 56 g 154 t 1 others

COMMENT:

```

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 730 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 381.
```

```

REFERENCE:      1 (bases 1 to 382)
AUTHOR (AU):    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE (TI):     National Cancer Institute, Cancer Genome Anatomy
                  Project (CGAP), Tumor Gene Index
JOURNAL (SO):   Unpublished (1997)
```

FEATURES (FEAT):

Feature Key	Location	Qualifier
-------------	----------	-----------

```

=====+=====+=====
source      1..382      /organism="Homo sapiens"
```

/db-xref="taxon:9606"
 /clone="IMAGE:2028991"
 /clone-lib="NCI-CGAP-Kid11"
 /lab-host="DH10B"
 /note="Organ: kidney; Vector:
 pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site-1: Not
 I; Site-2: Eco RI; Plasmid DNA
 from the normalized library
 NCI-CGAP-Kid3 was prepared, and ss
 circles were made in vitro.
 Following HAP purification, this
 DNA was used as tracer in a
 subtractive hybridization
 reaction. The driver was
 PCR-amplified cDNAs from a pool of
 5,000 clones made from the same
 library (cloneIDs 1322376-1323911,
 1456007-1456775, and
 1500552-1502855). Subtraction by
 Bento Soares and M. Fatima
 Bonaldo."

SEQUENCE (SEQ):

```

1 tttttttttt tttttttttt cctaagggtt aattttaact aatgaatttt aaatgatgaa
61 tgtaaagtca atccaagtct ttgcttattt gcaatgcaca aactattttt ttgtaacttg
121 caggggaaat acattctttt cacatgataa tgttttcgcc cttatttatg gtcttttatt
181 atttttcttg agtccttttc cttcaatagt ttaataagtc acttctggct tgtctagaga
241 gcaatcctag cacaataatg tttcaacttg caaggaaaaa cgcccttatt gagttgatag
301 aactcacaca cagcccccct tgggggtttt attttttaa aggaaaaatt tcccggttgg
361 ggggttttna aaaaaaaaaa aa
  
```

L6 ANSWER 129 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AF076619 GenBank (R)
 GenBank ACC. NO. (GBN): AF076619
 GenBank VERSION (VER): AF076619.1 GI:3650499
 CAS REGISTRY NO. (RN): 216295-93-1
 SEQUENCE LENGTH (SQL): 1950
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Rodents
 DATE (DATE): 26 Sep 1998
 DEFINITION (DEF): Rattus norvegicus molecular adapter rGrb14 (
 Grb14) mRNA, complete cds.
 SOURCE: Norway rat.
 ORGANISM (ORGN): Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Rodentia;
 Sciurognathi; Muridae; Murinae; Rattus
 NUCLEIC ACID COUNT (NA): 546 a 460 c 500 g 444 t
 REFERENCE: 1 (bases 1 to 1950)
 AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
 Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
 Burnol,A.F.
 TITLE (TI): Identification of the rat adapter ***Grb14*** as an
 inhibitor of insulin actions
 JOURNAL (SO): J. Biol. Chem., 273 (40), 26026-26035 (1998)
 OTHER SOURCE (OS): CA 130:20710
 REFERENCE: 2 (bases 1 to 1950)
 AUTHOR (AU): Kasus-Jacobi,A.; Perdereau,D.; Burnol,A.-F.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (03-JUL-1998) UPR 1524, CNRS, 9 rue Jules
 Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1950	/organism="Rattus norvegicus" /strain="Wistar"
gene	1..1950	/db-xref="taxon:10116" /gene="Grb14"
CDS	70..1686	/gene="Grb14" /note="signal transduction protein; Grb7 family member; binds the insulin receptor" /codon-start=1

```

/product="molecular adapter
rGrb14"
/protein-id="AAC61478.1"
/db-xref="GI:3650500"
/translation="MTTSLQDQSAAGRAGAQDS
PLAVQVCRAVQKGDAQDPAQVPG
LHALSPASDATRRGAMDRRKAKDLEVQETPSIPN
PFPELCCSPLTSVLSAGLFPRSNS
RKKQVIKVSSEDETSRALEVPSDVTARDVCQLLI
LKNHYVDDNSWTLFEHLSHTGVER
TVEDHELLTEVLSHWMEEDNKLYLRKNYAKYEF
FKNPMYFFPEHMFVSFATEMNGDRS
LTQIPQVFLSSNTYPEIHGFLHAKEQGKKSWKKA
YFFLRRLSGLYFSTKGTSKEPRHLQ
FFSEFSTSNVYMSLAGKKKHGAPTGYGFCFKPTK
AGGPRDLKMLCAEEDQSRMCWTA
IRLLKYGMQLYQNYMHPSQARSACSSQSVSPMRS
VSENSLVAMDFSGQKTRVIDNPTE
ALSVAVEEGLAWRKKGLRLGNHGSPTAPSQSSA
VNMAHRSQPWFHHRISRDEAQQ
ITRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIK
HFQIIPVEDDGEVFTLDDGHTKF
TDLIQLVEFYQLNKGVLCKLKHVCARMAV"

```

SEQUENCE (SEQ):

```

1 gctggacccc agccttttctt cgctttcgcc tcgcggtcga tgactcccta gaccccttgg
61 cctacgatca tgaccacgtc cctgcaagat gggcagagcg ccgcgggccc ggcggggccc
121 caggactccc cgctggcagt gcaggtgtgc cgcgttgccc agggcaaggg agacgccagc
181 gacccggctc aggtcccccgg actgcacgcg ctgtccccgg cctcagatgc gacccggcgc
241 ggtgccatgg acaggagaaa agcgaaagat ctggaagtgc aggaacgcc ttccattcct
301 aaccccttcc ctgagctctg ctgttctcca cttacatcgg tgctgtcagc aggcctcttc
361 cccagatcaa attcaaggaa gaaacaggtg attaaagtgt acagcgagga tgagaccagc
421 agagcggttag aggtgcccag tgacgtcaca gcccgtgatg tctgccagct gttgatcctg
481 aagaaccact atgtcgacga caatagctgg accctttttg agcacctgtc tcacacaggg
541 gtagaaagga cagtggagga ccatgagctg ctgactgaag tgctgtctca ttgggtgatg
601 gaagaagata ataagctgta tcttagaaag aattatgcca aatatgaatt ttttaagaac
661 ccaatgtatt tctttccaga gcacatgggtg tcttttgcaa ctgaaatgaa cggtgacaga
721 tcccttacac agatcccgcg ggtgttttta agctcaaaca catatcctga aatccatggc
781 ttctctgcatg caaaggaaca ggggaagaag tcttgaaaaa aagcttactt ttttctcaga
841 agatctgggtt tataatttttc tactaaaggc acatccaagg aaccacggca cttgcagtgt
901 ttcagtgaat tcagcactag taatgtttac atgtcactgg caggcaaaaa aaagcatgga
961 gcgccgactc cctatggatt ctgctttaag cctaccaaaag caggaggggc ccgggacctg
1021 aaaatgctgt gtgcagaaga agaccaaagc aggatgtgct ggggtgaccgc cattagattg
1081 ctcaagtatg gcatgcagct ctaccagaat tatatgcac ccatcccaagc tagaagcgcc
1141 tgcagttctc agagcgtatc acctatgaga agcgtatcag agaattccct agtagcaatg
1201 gacttctcag gtcagaagac cagagtcata gacaacccca ctgaagccct ttcggttgcc
1261 gttgaggaag gactcgcttg gaggaaaaaa ggatgtttac gcctggggaa tcatgggagt
1321 cccactgcgc cctctcagag ctctgctgtg aacatggctc tccaccgggc ccagccatgg
1381 tttcaccaca gaatttctag agatgaagct cagcagttga ttaccgggca ggggcctgtg
1441 gatggagttt tcttggtacg ggatagtcag agtaacccca gaacttttgt actgtcaatg
1501 agtcacggag aaaagataaa acactttcaa attatacccg tggagatga tggtagggtg
1561 ttccacaccc tggatgatgg ccatacgaag ttcacagatc tcatccagct cgtggagttc
1621 taccagctca acaagggggg ccttccttgc aagctgaagc attactgtgc taggatggct
1681 gtttagccaa actgtctgtg actcgttaaa ctatggaaga tggaggatgc aaagaagaat
1741 gattagagag agagagagag agagagagag agagagagag agagaggaga
1801 tcacaaggct ggaacaaaat catggtgaaa agaagattca cctgtgggtt acaaaaaaat
1861 aggtcacgta ttgcaaatta gtgaagactt ggattcgtat tactctcgtt actttaaat
1921 tattagttaa aattaaacct tattaataaa

```

L6 ANSWER 130 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

```

LOCUS (LOC): AI094433 GenBank (R)
GenBank ACC. NO. (GBN): AI094433
GenBank VERSION (VER): AI094433.1 GI:3433409
CAS REGISTRY NO. (RN): 392191-42-3
SEQUENCE LENGTH (SQL): 420
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 10 Nov 1998
DEFINITION (DEF): ou87b07.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens
cDNA clone IMAGE:1634773 3' similar to TR:Q14449 Q14449
***GRB14*** . ;, mRNA sequence.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;

```


Hominidae; Homo
NUCLEIC ACID COUNT (NA): 115 a 75 c 67 g 163 t
COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 796 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 277.

REFERENCE: 1 (bases 1 to 420)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..420	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1634773" /clone-lib="Soares-NSF-F8-9W-OT-PA -P-S1" /lab-host="DH10B" /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

SEQUENCE (SEQ):

```
1 cctaaggttt aattttaact aatgaatttt aaatgatgaa tgtaaagtca atccaagtct
61 ttgcttattt gcaatgcaca aactattttt ttgtaacttg caggtgaaat acattctttt
121 cacatgataa cgttttcgcc cttatttatg gtcttttatt atttttcttg agtccttttc
181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg
241 ttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag
301 atctgtaaat cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
361 tgggtataatt tgaaagtgct ttattttttg tccatgactc attgacagta cgaaagtttt
```

L6 ANSWER 131 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AA917917 GenBank (R)
GenBank ACC. NO. (GBN): AA917917
GenBank VERSION (VER): AA917917.1 GI:3057807
CAS REGISTRY NO. (RN): 206814-02-0
SEQUENCE LENGTH (SQL): 497
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 10 Jun 1998
DEFINITION (DEF): ol76g09.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone
IMAGE:1535584 3' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 136 a 95 c 79 g 187 t

COMMENT:

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 664 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 440.

REFERENCE: 1 (bases 1 to 497)
AUTHOR (AU): NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE (TI): National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
JOURNAL (SO): Unpublished (1997)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..497	/organism="Homo sapiens" /db-xref="taxon:9606" /clone="IMAGE:1535584" /clone-lib="NCI-CGAP-Kid3" /lab-host="DH10B" /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

SEQUENCE (SEQ):

```
1 catttttttc ctaagggttta attttaacta atgaatttta aatgatgaat gtaaagtcaa
61 tccaagtctt tgcttatttg caatgcacaa actatttttt tgtaacttgc aggtgaaata
121 cattcttttc acatgataat gttttcgccc ttatttatgg tcttttatta tttttcttga
181 gtccttttcc ttcaatagtt taataagtca cttctggcct gtctagagag caatcctagc
241 acaataatgt ttcaacttgc aaggaagaac gcccttattg agttgataga actccaccag
301 ctgtattaga tctgtaaatc ttgtgtggcc atcatccagt gtgtggaaca tttcaccgtc
361 atcttctact ggtataattt gaaagtgtct tattttctgt ccatgactca ttgacagtac
421 gaaagttttg gggttactct gactatcccc taccaagaaa actcatccac aagtccttgc
481 tgaataatca atcgctg
```

L6 ANSWER 132 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AA684351 GenBank (R)
GenBank ACC. NO. (GBN): AA684351
GenBank VERSION (VER): AA684351.1 GI:2670937
CAS REGISTRY NO. (RN): 200792-61-6
SEQUENCE LENGTH (SQL): 503
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 9 Dec 1997
DEFINITION (DEF): vm69d04.s1 Knowles Solter mouse 2 cell Mus musculus
cDNA clone IMAGE:1003495 5' similar to TR:Q14449 Q14449
GRB14 . ;, mRNA sequence.
SOURCE: house mouse.

ORGANISM (ORGN): Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 127 a 121 c 135 g 120 t

COMMENT:

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:567711
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 459.

REFERENCE: 1 (bases 1 to 503)

AUTHOR (AU): Marra,M.; Hillier,L.; Allen,M.; Bowles,M.; Dietrich,N.;
Dubuque,T.; Geisel,S.; Kucaba,T.; Lacy,M.; Le,M.;
Martin,J.; Morris,M.; Schellenberg,K.; Steptoe,M.;
Tan,F.; Underwood,K.; Moore,B.; Theising,B.; Wylie,T.;
Lennon,G.; Soares,B.; Wilson,R.; Waterston,R.

TITLE (TI): The WashU-HHMI Mouse EST Project

JOURNAL (SO): Unpublished (1996)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..503	/organism="Mus musculus" /strain="B6D2 F1/J" /db-xref="taxon:10090" /clone="IMAGE:1003495" /clone-lib="Knowles Solter mouse 2 cell" /tissue-type="embryo" /dev-stage="2-cell" /lab-host="DH10B" /note="Organ: embryo; Vector: pBluescribe (modified); Site-1: MluI; Site-2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTT T-3'. cDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

SEQUENCE (SEQ):

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361 agatgatggt gagctgttcc atactctgga tgatggccat acgaagttca cagacctcat
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481 ctgtgctagg atggctgttt agc
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L6 ANSWER 133 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSU69276 GenBank (R)
GenBank ACC. NO. (GBN): U69276
GenBank VERSION (VER): U69276.1 GI:1546834
CAS REGISTRY NO. (RN): 181109-72-8
SEQUENCE LENGTH (SQL): 2504
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 17 Sep 1996
DEFINITION (DEF): Human hGrbIRbeta/hGrb10 (GRBIRbeta/GRB10) mRNA,
complete cds.
SOURCE: human.

ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 639 a 652 c 654 g 555 t 4 others

REFERENCE: 1 (bases 1 to 2504)

AUTHOR (AU): Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
 Shoelson,S.E.

TITLE (TI): Human GrbIRbeta/Grb10: Splice Variants of an Insulin
 and Growth Factor Receptor-Binding Protein with PH and
 SH2 Domains

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 2504)

AUTHOR (AU): Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
 Shoelson,S.E.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (04-SEP-1996) Research Division, Joslin
 Diabetes Center, One Joslin Place, Boston, MA 02215,
 USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2504	/organism="Homo sapiens" /db-xref="taxon:9606" /tissue-type="cerebellum and skeletal muscle"
gene	1..2504	/gene="GRBIRbeta/GRB10"
CDS	288..1898	/gene="GRBIRbeta/GRB10" /note="signal transduction protein containing PH and SH2 domains and a potential SH3 domain interaction site; insulin receptor binding protein, binds the insulins, PDGF, and EGF receptors; splice variant of hGrbIR; member of the Grb7/Grb10/Grb14 family" /codon-start=1 /product="hGrbIRbeta/hGrb10" /protein-id="AAB08431.1" /db-xref="GI:1546835" /translation="MNASLESLSYACSMQSDTVP LLQNGQHARSQPRASGPPRSIQPQ VSPRQRVQRSQPVHILAVRRLQEEDQQFRTSSLP AIPNPFPELCGPGSPPVLTGSLP PSQAAAKQDVKFSEDDGTSKVVEILADMTARDLC QLLVYKSHCVDDNSWTLVEHHPHL GLERCLEDHELVVQVESTMASESFLFRKNYAKY EFFKNPMNFFPEQMVTWCQQSNGS QTQLLQNFNLSSSCPEIQGFLHVKELGKKS WKKL YVCLRRSGLYCSTKGTSKEPRHLQ LLADLEDSNIFSLIAGRKQYNAPT DHGLCIKPNK VRNETKELRLLCAEDEQTRTCWMT AFRLLKYEMLLYQNYRIPQQRKALLSPFSTPVRS VSENSLVAMDFSGQTGRVIENPAE AQSAALEEGHAWRKRSTRMNLGQSPLHPSTLS TVIHRTQHWFHGRFSREESHRIIK QQGLVDGLFLLRDSQSNPKAFVLTLC HHQKIKNF QILPCEDDQQTFFSLDDGNTKFS LIQLVDFYQLNKGVL PCKLKHH CIRVAL"

SEQUENCE (SEQ):

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L6 ANSWER 134 OF 135 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HUMGRB14R GenBank (R)
GenBank ACC. NO. (GBN): L76687
GenBank VERSION (VER): L76687.1 GI:1369836
CAS REGISTRY NO. (RN): 391791-70-1
SEQUENCE LENGTH (SQL): 2376
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 6 May 1998
DEFINITION (DEF): Homo sapiens ***Grb14*** mRNA, complete cds.
SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 631 a 652 c 583 g 510 t
REFERENCE: 1 (bases 1 to 2376)
AUTHOR (AU): Daly,R.J.; Sanderson,G.M.; Janes,P.W.; Sutherland,R.L.
TITLE (TI): Cloning and characterization of ***GRB14*** , a
novel member of the GRB7 gene family
JOURNAL (SO): J. Biol. Chem., 271 (21), 12502-12510 (1996)
OTHER SOURCE (OS): CA 125:27254

FEATURES (FEAT):

Feature Key	Location	Qualifier
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gene	1..2376	/gene="Grb14"
5'UTR	1..540	/gene="Grb14"
CDS	541..2163	/gene="Grb14" /codon-start=1 /protein-id="AAC15861.1" /db-xref="GI:1369837" /translation="MTTSLQDQGSAAASRAAARDS PLAAQVCGAAQGRGDAHD LAPAPW LHARALLPLPDGTRGCAADRRKKKDLDPPEMPSI PNPFPELCCSPITSVLSDLFPKA NSRKKQVIKVYSEDETSRALDVPSDITARDVCQL LILKNHYIDHSWTLFEHLPHIGV ERTIEDHELVIIEVLSNWGIEEENKLYFRKNYAKY EFFKNPMYFFPEHMSVFATETNGE ISPTQILQMFLSSSTYPEIHGFLHAKEQGKKS WK KIYFFLRRLSGLYFSTKGTSKEPRH LQFFSEFGNSDIYVSLAGKKKHGAPTNYGFCFKP

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L6 ANSWER 135 OF 135 CONFSCI COPYRIGHT 2004 CSA on STN
AN 1999:27349 CONFSCI
DN 99-039843
TI Novel FGF signaling pathway u ***Grb14*** binds to FGF receptor 1
AU Reilly, J.F.; Mickey, G.; Maher, P.A.
CS Dep. Cell Biol., Scripps Res. Inst., La Jolla, CA 92037, USA
SO American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD
20814, USA; phone: (301) 530-7153; fax: (301) 530-7139; email:
ascbinfo@ascb.org; URL: www.ascb.org/ascb/, Abstracts available. Price
\$45. Paper No. 1365.
Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual
Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad,
Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance,
Mark-Rambar Family Foundation.
DT Conference
FS DCCP
LA English
STN INTERNATIONAL LOGOFF AT 15:35:54 ON 05 JAN 2004